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OM protein - protein search, using sw model

Run on: September 1, 2005, 16:25:44 ; Search time 43 Seconds
(without alignments)

22.568 Million cell updates/sec

Title: US-09-993-366-1

Perfect score: 66

Sequence: 1 KLVPFATLHERL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.psp.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.psp.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.psp.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.psp.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.psp.*

6: /cgn2_6/ptodata/1/iaa/backfiles.psp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	382	4	US-09-800-729-206
2	66	100.0	396	4	US-09-800-729-207
3	66	100.0	397	4	US-09-079-030-123
4	66	100.0	426	4	US-09-949-016-10854
5	38	57.6	243	4	US-09-543-681A-4422
6	38	57.6	492	4	US-09-489-039A-14208
7	38	57.6	850	4	US-09-949-016-11324
8	37	56.1	90	4	US-09-540-236-3521
9	37	56.1	127	4	US-08-311-731A-226
10	37	56.1	161	4	US-09-270-767-33980
11	37	56.1	161	4	US-09-270-767-49197
12	37	56.1	193	4	US-09-949-016-10446
13	37	56.1	302	4	US-09-902-540-10445
14	37	56.1	339	3	US-08-758-280-1
15	37	56.1	339	3	US-08-758-280-2
16	37	56.1	339	3	US-08-964-614A-1
17	37	56.1	339	3	US-08-964-614A-2
18	37	56.1	339	4	US-09-538-092-1274
19	37	56.1	436	4	US-09-724-623-94
20	37	56.1	436	4	US-09-902-540-16282
21	37	56.1	445	4	US-09-634-238-273
22	37	56.1	467	4	US-09-252-991A-25450
23	37	56.1	623	4	US-09-489-039A-11811
24	37	56.1	705	2	US-08-663-566A-19
25	37	56.1	705	2	US-08-023-610-19
26	37	56.1	705	2	US-08-288-065A-19
27	37	56.1	705	2	US-08-362-240A-19

28	56.1	705	5	PCT-US95-10245-19	Sequence 19, Appl
29	56.1	862	4	US-09-248-796A-16013	Sequence 16013, A
30	56.1	1051	4	US-09-252-991A-16989	Sequence 16989, A
31	56.1	1162	2	US-08-663-566A-15	Sequence 15, Appl
32	56.1	1162	2	US-08-023-610-15	Sequence 15, Appl
33	56.1	1162	2	US-08-288-065A-15	Sequence 15, Appl
34	56.1	1162	2	US-08-362-240A-15	Sequence 15, Appl
35	56.1	1162	5	PCT-US95-10245-15	Sequence 15, Appl
36	56.1	1265	3	US-09-347-878-5	Sequence 5, Appl
37	56.1	1265	3	US-09-347-878-7	Sequence 7, Appl
38	56.1	1265	4	US-08-980-326-2	Sequence 2, Appl
39	56.1	1265	4	US-08-980-326-74	Sequence 74, Appl
40	54.5	527	4	US-09-489-039A-14144	Sequence 14144, A
41	54.5	715	4	US-09-902-540-12939	Sequence 12939, A
42	54.5	739	3	US-08-510-646B-33	Sequence 33, Appl
43	53.0	141	4	US-09-270-767-35522	Sequence 35522, A
44	53.0	141	4	US-09-270-767-50739	Sequence 50739, A
45	53.0	143	3	US-09-134-001C-2941	Sequence 2941, Ap
46	53.0	143	4	US-09-710-279-54	Sequence 54, Appl
47	53.0	143	4	US-09-710-279-2672	Sequence 2672, Ap
48	53.0	199	4	US-09-248-796A-20525	Sequence 20525, A
49	53.0	377	4	US-09-248-796A-20227	Sequence 20227, A
50	53.0	473	4	US-08-985-343-6	Sequence 6, Appl
51	53.0	475	3	US-08-274-121B-4	Sequence 4, Appl
52	53.0	476	2	US-08-569-150A-3	Sequence 3, Appl
53	53.0	476	4	US-09-171-937C-2	Sequence 2, Appl
54	53.0	583	4	US-09-902-540-14460	Sequence 14460, A
55	53.0	669	4	US-09-107-532A-6532	Sequence 6532, Ap
56	53.0	676	4	US-09-902-540-10948	Sequence 10948, A
57	53.0	720	4	US-09-328-352-4435	Sequence 4435, Ap
58	51.5	1033	4	US-09-252-991A-20611	Sequence 20611, A
59	51.5	105	4	US-09-727-739B-36	Sequence 36, Appl
60	51.5	200	3	US-08-952-796-15	Sequence 15, Appl
61	51.5	203	4	US-09-902-540-10232	Sequence 10232, A
62	51.5	243	4	US-09-079-030-119	Sequence 119, App
63	51.5	256	1	US-08-594-808B-7	Sequence 7, Appl
64	51.5	267	1	US-07-959-946-3	Sequence 3, Appl
65	51.5	267	1	US-08-333-577-3	Sequence 3, Appl
66	51.5	267	3	US-08-952-796-2	Sequence 2, Appl
67	51.5	267	4	US-08-940-136-260	Sequence 260, App
68	51.5	267	4	US-09-919-039-27	Sequence 27, Appl
69	51.5	267	5	PCT-US92-08634-3	Sequence 3, Appl
70	51.5	382	4	US-09-492-709A-299	Sequence 299, App
71	51.5	682	4	US-09-270-767-45039	Sequence 45039, A
72	51.5	747	4	US-09-824-574-6	Sequence 6, Appl
73	51.5	753	4	US-09-949-016-10892	Sequence 10892, A
74	51.5	877	3	US-08-911-853-31	Sequence 31, Appl
75	51.5	877	3	US-09-479-409-31	Sequence 31, Appl
76	51.5	877	3	US-09-479-453-31	Sequence 31, Appl
77	51.5	1041	3	US-08-898-978-2	Sequence 2, Appl
78	51.5	1041	3	US-09-372-858-2	Sequence 2, Appl
79	51.5	1101	3	US-09-770-170-8	Sequence 8, Appl
80	50.0	93	4	US-09-621-976-4320	Sequence 4320, Ap
81	50.0	108	4	US-09-668-262A-6	Sequence 6, Appl
82	50.0	133	4	US-09-252-991A-18025	Sequence 18025, A
83	50.0	136	4	US-09-270-767-47225	Sequence 47225, A
84	50.0	151	3	US-08-679-493A-74	Sequence 74, Appl
85	50.0	189	4	US-09-583-110-5176	Sequence 5176, Ap
86	50.0	203	4	US-09-252-991A-26395	Sequence 26395, A
87	50.0	211	4	US-09-774-639-153	Sequence 153, App
88	50.0	223	4	US-09-270-767-42708	Sequence 42708, A
89	50.0	231	4	US-09-107-433-5068	Sequence 5068, Ap
90	50.0	261	4	US-09-583-110-5270	Sequence 5270, Ap
91	50.0	276	4	US-09-107-433-2780	Sequence 2780, Ap
92	50.0	316	4	US-09-328-352-6935	Sequence 6935, Ap
93	50.0	386	4	US-09-902-540-10982	Sequence 10982, A
94	50.0	391	4	US-09-800-729-208	Sequence 208, App
95	50.0	399	4	US-09-107-532A-4714	Sequence 4714, Ap
96	50.0	400	4	US-09-252-991A-3213	Sequence 3213, A
97	50.0	414	4	US-09-949-016-6906	Sequence 6906, Ap
98	50.0	419	4	US-09-252-991A-30457	Sequence 30457, A
99	50.0	421	4	US-09-668-262A-16	Sequence 16, Appl
100	50.0	423	4	US-09-668-262A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-800-729-206
; Sequence 206, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 206
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-206

Query Match 100.0%; Score 66; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 2

US-09-800-729-207
; Sequence 207, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 207
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-207

Query Match 100.0%; Score 66; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 3

US-09-079-030-123
; Sequence 123, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.

; APPLICANT: Hoogveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/079,030
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabesla R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-123

Query Match 100.0%; Score 66; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPFATELHERL 13
Db 30 KLVPFATELHERL 42

RESULT 4

US-09-949-016-10854
; Sequence 10854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10854
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10854

Query Match 100.0%; Score 66; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 109 KLVPFATELHERL 121

RESULT 5

US-09-543-681A-4422
; Sequence 4422, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4422
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4422

Query Match 57.6%; Score 38; DB 4; Length 243;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PFATELHE 11
Db 59 PFATELHE 66

RESULT 6

US-09-489-039A-14208
; Sequence 14208, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14208
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14208

Query Match 57.6%; Score 38; DB 4; Length 492;
Best Local Similarity 63.6%; Pred. No. 56;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LVFPATELHER 12
Db 152 LVFPATELHER 162

RESULT 7

US-09-949-016-11324
; Sequence 11324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11324
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11324

Query Match 57.6%; Score 38; DB 4; Length 850;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLVPFATELHE 11
Db 373 KLVPFATELHE 383

RESULT 8

US-09-540-236-3521
; Sequence 3521, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAT
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3521
; LENGTH: 90
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3521

Query Match 56.1%; Score 37; DB 4; Length 90;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PFATELHER 12
Db 22 PFATELHER 30

RESULT 9

US-08-311-731A-226
; Sequence 226, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
; US-08-311-731A-226

Query Match 56.1%; Score 37; DB 4; Length 127;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VPFATELHERL 13
Db 33 VPEAVSVHRR 43

RESULT 10
US-09-270-767-33980
; Sequence 33980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33980
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-33980

Query Match 56.1%; Score 37; DB 4; Length 161;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 3; Indels 1; Gaps 0;

QY 2 LVPPATELHE 11
Db 99 LEPYSTELHQ 108

RESULT 11
US-09-270-767-49197
; Sequence 49197, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49197
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49197

Query Match 56.1%; Score 37; DB 4; Length 161;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 3; Indels 1; Gaps 0;

QY 2 LVPPATELHE 11
Db 99 LEPYSTELHQ 108

RESULT 12
US-09-949-016-10446
; Sequence 10446, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10446
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-10446

Query Match 56.1%; Score 37; DB 4; Length 193;
Best Local Similarity 56.2%; Pred. No. 31;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPF-----ATELHER 12
Db 96 KLVPMGFTTATEFHQR 111

RESULT 13
US-09-902-540-10445
; Sequence 10445, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldkman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10445
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10445
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Query Match 56.1%; Score 37; DB 4; Length 302;
Best Local Similarity 66.7%; Pred. No. 50;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPPATELH 10
|-.| | | | |
Db 226 LIPLATQLH 234

RESULT 14
US-08-758-280-1
; Sequence 1, Application US/08758280
; Patent No. 6037125
; GENERAL INFORMATION:
; APPLICANT: Hasty, Paul
; TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN Rad51
; TITLE OF INVENTION: PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE WITH
; TITLE OF INVENTION: MAMMALIAN Rad51 FOR HINDERING CELL PROLIFERATION AND/OR
; TITLE OF INVENTION: VIABILITY OF PROLIFERATING CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,280
; FILING DATE: concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8535-013-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-758-280-1

Query Match 56.1%; Score 37; DB 3; Length 339;
Best Local Similarity 56.2%; Pred. No. 57;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPF----ATELHER 12
| | | | | | | | | |
Db 80 KLVPMGFTTATEFHQR 95

RESULT 15
US-08-758-280-2
; Sequence 2, Application US/08758280
; Patent No. 6037125
; GENERAL INFORMATION:
; APPLICANT: Hasty, Paul
; TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN Rad51
; TITLE OF INVENTION: PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE WITH

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,280
; FILING DATE: 05-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8535-0019-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6057104e
; US-08-964-614A-1

Query Match 56.1%; Score 37; DB 3; Length 339;
Best Local Similarity 56.2%; Pred. No. 57;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPF----ATELHER 12
   ||||| |||||
DB 80 KLVPMGFTTATEFHQR 95

RESULT 17
US-08-964-614A-2
; Sequence 2, Application US/08964614A
; Patent No. 6057104
; GENERAL INFORMATION:
; APPLICANT: Hascy, Paul
; TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN
; TITLE OF INVENTION: Rad51 PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE
; TITLE OF INVENTION: WITH MAMMALIAN Rad51 FOR HINDERING CELL PROLIFERATION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,614A
; FILING DATE: 05-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,280
; FILING DATE: 05-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8535-0019-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6057104e

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Db 380 FVTRLHERL 388
| | | | |

RESULT 20

US-09-902-540-16282
; Sequence 16282, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16282
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16282

Query Match 56.1%; Score 37; DB 4; Length 436;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PFATELHERL 13
| | | | |
Db 283 PFPELHDAI 292

RESULT 21

US-09-634-238-273
; Sequence 273, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christenson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 273
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-273

Query Match 56.1%; Score 37; DB 4; Length 445;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FATELHERL 13
| | | | |
Db 387 FVTRLHERL 395

RESULT 22

US-09-252-991A-25450
; Sequence 25450, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25450
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25450

Query Match 56.1%; Score 37; DB 4; Length 467;
Best Local Similarity 53.8%; Pred. No. 81;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLVPPFATELHERL 13
| | | | |
Db 60 KVMKHAELHERI 72

RESULT 23

US-09-489-039A-11811
; Sequence 11811, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11811
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11811

Query Match 56.1%; Score 37; DB 4; Length 623;
Best Local Similarity 54.5%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VPFATELHERL 13
| | | | |
Db 366 VPFGVEVHRV 376

RESULT 24

US-08-663-566A-19
; Sequence 19, Application US/08663566A
; Patent No. 5853733
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York

```
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/663,566A
; FILING DATE: June 13, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-663-566A-19
;
Query Match 56.1%; Score 37; DB 2; Length 705;
Best Local Similarity 54.3%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPFATLHERL 13
Db 316 IFFATOLQARI 326

RESULT 25
US-08-023-610-19
; Sequence 19, Application US/08023610
; Patent No. 5928648
; GENERAL INFORMATION:
; APPLICANT: Cochran Ph.D., Richard D
; APPLICANT: Macdonald Ph.D., Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys
; TITLE OF INVENTION: and Uses Thereof
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 amino acids
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```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-023-610-19
;
Query Match 56.1%; Score 37; DB 2; Length 705;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPFATLHERL 13
Db 316 IFFATOLQARI 326

RESULT 26
US-08-288-065A-19
; Sequence 19, Application US/08288065A
; Patent No. 5961982
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D
; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-
; TITLE OF INVENTION: HVT-050 and Uses Thereof
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,065A
; FILING DATE: Aug-09-94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-288-065A-19
;
Query Match 56.1%; Score 37; DB 2; Length 705;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPFATLHERL 13
Db 316 IFFATOLQARI 326

RESULT 27
US-08-362-240A-19
; Sequence 19, Application US/08362240A
; Patent No. 5965138
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
```

APPLICANT: Junker, David
APPLICANT: Wild, Martha A
TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/362,240A
APPLICATION NUMBER: US/08/362,240A
FILING DATE: Dec-22-94
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-362-240A-19
Query Match 56.1%; Score 37; DB 2; Length 705;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 3 VPFPATELHERL 13
Db 316 IPFATQLQARI 326
RESULT 28
PCT-US95-10245-19
Sequence 19, Application PC/TUS9510245
GENERAL INFORMATION:
APPLICANT: SYNTRO CORPORATION
TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10245
FILING DATE: 09-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
TELEX: 422523
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-10245-19
Query Match 56.1%; Score 37; DB 5; Length 705;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 3 VPFPATELHERL 13
Db 316 IPFATQLQARI 326
RESULT 29
US-09-248-796A-16013
Sequence 16013, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16013
LENGTH: 862
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-16013
Query Match 56.1%; Score 37; DB 4; Length 862;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 LVFPATELHE 11
Db 60 LVEPLTEIHE 69
RESULT 30
US-09-252-991A-16989
Sequence 16989, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16989
LENGTH: 1051
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16989

Query Match 56.1%; Score 37; DB 4; Length 1051;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVPFATELHER 12
:|||||:
Db 949 IVEFAKELHEQ 959

RESULT 31

US-08-663-566A-15
; Sequence 15, Application US/08663566A

; Patent No 5853733

; GENERAL INFORMATION:

; APPLICANT: Cochran, Mark D

; APPLICANT: Macdonald, Richard D

; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

; TITLE OF INVENTION: and Uses Thereof

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/663,566A

; FILING DATE: June 13, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P

; REGISTRATION NUMBER: 28,678

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)278-0400

; TELEFAX: (212)391-0526

; TELEX: 422523

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1162 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-663-566A-15

Query Match 56.1%; Score 37; DB 2; Length 1162;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPFATELHERL 13
:|||||:
Db 769 IPFATOLQARI 779

RESULT 32

US-08-023-610-15

; Sequence 15, Application US/08023610

; Patent No. 5928648

; GENERAL INFORMATION:

; APPLICANT: Cochran Ph.D, Mark D

; APPLICANT: Macdonald Ph.D., Richard D

; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys

; TITLE OF INVENTION: and Uses Thereof

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/023,610
; FILING DATE: February 26, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq, John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-023-610-15

Query Match 56.1%; Score 37; DB 2; Length 1162;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPFATELHERL 13
:|||||:
Db 769 IPFATOLQARI 779

RESULT 33

US-08-288-065A-15

; Sequence 15, Application US/08288065A

; Patent No. 5961982

; GENERAL INFORMATION:

; APPLICANT: Cochran, Mark D

; APPLICANT: Macdonald, Richard D

; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys S-

; TITLE OF INVENTION: HVT-050 and Uses Thereof

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/288,065A

; FILING DATE: Aug-09-94

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)278-0400

; TELEFAX: (212)391-0526

; TELEX: 422523

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1162 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-288-065A-15

Query Match 56.1%; Score 37; DB 2; Length 1162;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPFATELHERL 13
Db 769 IFFATLQARI 779

RESULT 34

US-08-362-240A-15
; Sequence 15, Application US/08362240A

; Patent No. 5965138

; GENERAL INFORMATION:

; APPLICANT: Cochran, Mark D

; APPLICANT: Junker, David

; APPLICANT: Wild, Martha A

; TITLE OF INVENTION: Recombinant Herpesvirus and Uses Thereof

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/362,240A

; FILING DATE: Dec-22-94

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P

; REGISTRATION NUMBER: 28,678

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)278-0400

; TELEFAX: (212)391-0526

; TELEX: 422523

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1162 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-362-240A-15

Query Match 56.1%; Score 37; DB 2; Length 1162;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPFATELHERL 13
Db 769 IFFATLQARI 779

RESULT 35

PCT-US95-10245-15

; Sequence 15, Application PC/TUS9510245

; GENERAL INFORMATION:

; APPLICANT: SYNTRO CORPORATION

; TITLE OF INVENTION: Recombinant Herpesvirus of Turkeys And Uses Thereof

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: John P. White

; STREET: 1185 Avenue of the Americas

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10245
; FILING DATE: 09-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; TELEX: 422523
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-10245-15

Query Match 56.1%; Score 37; DB 5; Length 1162;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPFATELHERL 13
Db 769 IFFATLQARI 779

RESULT 36

US-09-347-878-5

; Sequence 5, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES

; FILE REFERENCE: 25885-1651

; CURRENT APPLICATION NUMBER: US/09/347,878C

; CURRENT FILING DATE: 1999-07-06

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1265

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-347-878-5

Query Match 56.1%; Score 37; DB 3; Length 1265;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FATELHERL 13
Db 1137 FABELHERV 1145

RESULT 37

US-09-347-878-7

; Sequence 7, Application US/09347878C

; Patent No. 6376210

; GENERAL INFORMATION:

; APPLICANT: Yuan, Chong

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES

; FILE REFERENCE: 25885-1651

; CURRENT APPLICATION NUMBER: US/09/347,878C

; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-878-7

Query Match 56.1%; Score 37; DB 3; Length 1265;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FATELHERL 13
||| |||||
Db 1137 FAEELHERV 1145

RESULT 38
US-08-980-326-2

; Sequence 2, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003
; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1265
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: (1)...(1265)
; OTHER INFORMATION: Wild type methionine synthase polypeptide.
US-08-980-326-2

Query Match 56.1%; Score 37; DB 4; Length 1265;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FATELHERL 13
||| |||||
Db 1137 FAEELHERV 1145

RESULT 39
US-08-980-326-74

; Sequence 74, Application US/08980326
; Patent No. 6703197
; GENERAL INFORMATION:
; APPLICANT: Gravel, Roy A.
; APPLICANT: Rozen, Rima
; APPLICANT: LeClerc, Daniel
; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND CANCER
; FILE REFERENCE: 50004/002003

; CURRENT APPLICATION NUMBER: US/08/980,326
; CURRENT FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/050,310
; EARLIER FILING DATE: 1997-06-20
; EARLIER APPLICATION NUMBER: 60/031,964
; EARLIER FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 1265
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1265)
; OTHER INFORMATION: Mutant methionine synthases: 881
; OTHER INFORMATION: can be Ile or deleted; 919 can be Asp or Gly; 920
; OTHER INFORMATION: can be His or Asp.
US-08-980-326-74

Query Match 56.1%; Score 37; DB 4; Length 1265;
Best Local Similarity 77.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 FATELHERL 13
||| |||||
Db 1137 FAEELHERV 1145

RESULT 40

US-09-489-039A-14144
; Sequence 14144, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14144
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14144

Query Match 54.5%; Score 36; DB 4; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TELHERL 13
||| |||||
Db 111 TELHERL 117

RESULT 41

US-09-902-540-12939
; Sequence 12939, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10 (15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12939
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12939

Query Match 54.5%; Score 36; DB 4; Length 715;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LVPFATELHER 12
:|||||:
Db 570 LVPFAGSRHDR 580

RESULT 42

US-08-510-646B-33
; Sequence 33, Application US/08510646B
; Patent No. 6077699

; GENERAL INFORMATION:

; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: Zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; TITLE OF INVENTION: Coding For These Polypeptides And Their Use
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/510,646B
; FILING DATE: 03-AUG-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/403,852
; FILING DATE: 10-MAY-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR 93/00923
; FILING DATE: 25-SEP-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92/11441
; FILING DATE: 25-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03806.0054-01000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 739 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-510-646B-33

Query Match 54.5%; Score 36; DB 3; Length 739;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 KLVPF--ATELHERL 13
:|||||:
Db 267 RTVPFHLEPHERL 281

RESULT 43

US-09-270-767-35522
; Sequence 35522, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 35522
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-35522

Query Match 53.0%; Score 35; DB 4; Length 141;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VPPATELH 10
:|||||:
Db 40 IPFSSELH 47

RESULT 44

US-09-270-767-50739
; Sequence 50739, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 50739
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-50739

Query Match 53.0%; Score 35; DB 4; Length 141;
Best Local Similarity 62.5%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VPPATELH 10
:|||||:
Db 40 IPFSSELH 47

RESULT 45

US-09-134-001C-2941
; Sequence 2941, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

```

; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; CURRENT APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2941
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2941

Query Match      53.0%; Score 35; DB 3; Length 143;
Best Local Similarity 58.3%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 KLVPPFATLHER 12
Db      64 KLTFFLELEKR 75

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Search completed: September 1, 2005, 16:42:17
Job time : 45 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 16:23:14 ; Search time 39 Seconds
(without alignments)
32.072 Million cell updates/sec

Title: US-09-993-366-1

Perfect score: 66

Sequence: 1 KLVPPFATLHERL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:**

1: Piri:**

2: Pir2:**

3: Pir3:**

4: Pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	396	1 LPHU4	apolipoprotein A-I
2	66	100.0	401	2 A47141	apolipoprotein A-I
3	66	100.0	429	2 S29565	apolipoprotein A-I
4	41	62.1	261	2 AG3116	conserved hypotet
5	41	62.1	265	2 F98170	hypothetical prote
6	40	60.6	266	1 LPRB1Z	apolipoprotein A-I
7	39	59.1	241	2 A24998	apolipoprotein A-I
8	39	59.1	353	2 S70629	Rad51 homolog mei-
9	39	59.1	697	2 E96752	hypothetical prote
10	39	59.1	2796	2 JC4743	fatty-acid synthas
11	39	59.1	3069	2 H70656	fatty-acid synthas
12	39	59.1	3076	2 A87058	fatty acid synthas
13	38	57.6	317	2 G70313	lipopolysaccharide
14	38	57.6	391	1 LPR7A4	apolipoprotein A-I
15	38	57.6	405	2 C75567	adenylosuccinate s
16	38	57.6	428	2 D84153	adenylosuccinate s
17	38	57.6	432	2 G97653	adenylosuccinate s
18	38	57.6	432	2 AE2877	adenylosuccinate s
19	38	57.6	473	2 AD0747	alpha, alpha-trehal
20	38	57.6	543	2 F69501	acetolactate synth
21	38	57.6	589	2 E71251	probable oligoendo
22	38	57.6	847	2 T52436	RF28 protein - Ara
23	38	57.6	850	2 JC5047	ras GTPase-activat
24	38	57.6	983	1 TC2381	Glycine cleavage s
25	38	57.6	987	1 TQBS30	transposase - Baci
26	38	57.6	1456	2 T01397	LTR gag/pol polypr
27	38	57.6	1474	2 B85188	retrotransposon li
28	38	57.6	2088	2 E71436	hypothetical prote
29	37	56.1	222	2 T26500	peptidylprolyl iso

30	37	56.1	231	2 JQ0704	apolipoprotein A-I
31	37	56.1	259	2 A24700	apolipoprotein A-I
32	37	56.1	264	2 S31394	apolipoprotein A-I
33	37	56.1	265	2 A46018	apolipoprotein AI
34	37	56.1	265	2 JT0672	apolipoprotein A-I
35	37	56.1	289	2 C96752	probable DNA-bindi
36	37	56.1	339	2 S35642	RAD51 protein homo
37	37	56.1	339	2 I58295	RAD51 protein homo
38	37	56.1	339	2 A48221	RAD51 protein homo
39	37	56.1	394	2 S45881	probable purine nu
40	37	56.1	448	2 C83347	probable dipeptida
41	37	56.1	463	2 T38621	peptidyl prolyl ci
42	37	56.1	621	2 S37664	peptidic polypro
43	37	56.1	624	1 JC4510	pullulanase (EC 3.
44	37	56.1	630	2 S37663	peptidic polypro
45	37	56.1	1046	2 S39630	multidrug-efflux t
46	37	56.1	1046	2 E83593	RND multidrug effl
47	37	56.1	1134	1 VGIHIB	E2 glycoprotein pr
48	37	56.1	1162	1 VGIHAK	E2 glycoprotein pr
49	37	56.1	1162	2 S14940	E2 glycoprotein pr
50	37	56.1	1162	2 S14939	E2 glycoprotein pr
51	37	56.1	1162	2 S07421	E2 glycoprotein pr
52	37	56.1	1253	2 T42376	5-methyltetrahydro
53	37	56.1	1347	2 B90674	Aida-1 adhesin-lik
54	37	56.1	1349	2 E85524	probable beta-barr
55	36	54.5	162	2 S78127	NADH2 dehydrogenas
56	36	54.5	222	2 C86302	probable NADH-ubiq
57	36	54.5	222	2 S52380	NADH2 dehydrogenas
58	36	54.5	229	2 S52386	NADH2 dehydrogenas
59	36	54.5	229	2 S52385	NADH2 dehydrogenas
60	36	54.5	264	2 S60367	transcription fact
61	36	54.5	314	2 F83945	tRNA isopentenylpy
62	36	54.5	335	1 DEBSGF	glyceroldehyde-3-p
63	36	54.5	419	2 AH2403	adenylosuccinate s
64	36	54.5	454	2 T01400	translation elonga
65	36	54.5	464	2 AF0214	probable membrane
66	36	54.5	518	2 A85793	probable transport
67	36	54.5	518	2 E90944	conserved hypotet
68	36	54.5	518	2 A81865	conserved hypotet
69	36	54.5	518	2 C81077	hypothetical prote
70	36	54.5	519	2 H64942	probable membrane
71	36	54.5	519	2 AE0726	alpha-xylosidase -
72	36	54.5	764	2 A72394	hypothetical prote
73	36	54.5	879	2 AC2347	two-component hybr
74	36	54.5	935	2 AE2469	HIV-1 retropepsin
75	36	54.5	1053	1 GNLJBT	atrial natriuretic
76	36	54.5	1057	1 OYMSAR	atrial natriuretic
77	36	54.5	1057	1 OYRTR	guanylyl cyclase A
78	36	54.5	1057	2 I55319	natriuretic peptid
79	36	54.5	1057	2 I57963	protoporphyrin IX
80	36	54.5	1382	2 T01789	virginiamycin S sy
81	36	54.5	1997	2 T30874	CNA peptide synthe
82	36	54.5	7463	2 T36248	genome polyprotein
83	35.5	53.8	3344	2 JQ1899	abortive infection
84	35	53.0	89	2 I40752	apolipoprotein A-I
85	35	53.0	164	2 S21830	conserved hypotet
86	35	53.0	180	2 AC0056	hypothetical prote
87	35	53.0	256	2 C83474	apolipoprotein A-I
88	35	53.0	284	2 JC5456	apolipoprotein A-I
89	35	53.0	266	1 LPDGA1	ABC transporter (A
90	35	53.0	279	2 A11399	ABC transporter (A
91	35	53.0	279	2 AH1775	hypothetical prote
92	35	53.0	336	2 F90435	Xaa-Pro dipeptidas
93	35	53.0	363	1 G69869	exodeoxyribonuclea
94	35	53.0	394	2 G72212	probable acyl-CoA
95	35	53.0	401	2 T35956	trehalose-6-phosph
96	35	53.0	474	2 A85803	trehalose-6-phosph
97	35	53.0	474	2 D90954	alpha, alpha-trehal
98	35	53.0	474	2 T09754	catalase (EC 1.11.
99	35	53.0	492	2 T09754	alkyl hydroperoxid
100	35	53.0	521	1 B35441	

ALIGNMENTS

```

RESULT 1
LPHUA4
apolipoprotein A-IV precursor [validated] - human
N/Alternate names: apoA-IV
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text change 09-Jul-2004
C/Accession: A94137; A94059; A29330; A26280; I37177; C54223; A61203; A26481; S02
R;Karathanasis, S.K.; Oetgen, P.; Haddad, I.A.; Antonarakis, S.E.
Proc. Natl. Acad. Sci. U.S.A. 83, 8457-8461, 1986
A/Title: Structure, evolution, and polymorphisms of the human apolipoprotein A4 gene (AF
A/Reference number: A94137; MUID:87041474; PMID:3095836
A/Accession: A94137
A/Molecule type: DNA
A/Residues: 1-396 <KAR1>
A/Cross-references: UNIPROT:P06727; UNIPROT:Q13784; GB:M14642; NID:gl78760; PIDN:AAA5174
R;Karathanasis, S.K.
Proc. Natl. Acad. Sci. U.S.A. 82, 6374-6378, 1985
A/Title: Apolipoprotein multigene family: tandem organization of human apolipoprotein A
A/Reference number: A94059; MUID:86016704; PMID:3931073
A/Accession: A94059
A/Molecule type: mRNA
A/Residues: 135-378 <KAR2>
A/Cross-references: GB:M10373; NID:G563319; PIDN:AAB59516.1; PID:G563320
R;Karathanasis, S.K.; Yunis, I.
Biochemistry 25, 3962-3970, 1986
A/Title: Structure, evolution, and tissue-specific synthesis of human apolipoprotein AIV
A/Reference number: A24449; MUID:86296629; PMID:3755616
A/Accession: A24449
A/Molecule type: mRNA
A/Residues: 1-396 <KAR3>
A/Cross-references: GB:M13654; NID:gl78758; PIDN:AAA51744.1; PID:gl78759
R;Gordon, J.I.; Bisgaier, C.L.; Sims, H.F.; Sachdev, O.P.; Glickman, R.M.; Strauss, A.W.
J. Biol. Chem. 259, 468-474, 1984
A/Title: Biosynthesis of human preapolipoprotein A-IV.
A/Reference number: A92475; MUID:84161950; PMID:6706947
A/Contents: annotation; signal sequence cleavage site
R;Elshourbagy, N.A.; Walker, D.W.; Paik, Y.K.; Boguski, M.S.; Freeman, M.; Gordon, J.I.;
J. Biol. Chem. 262, 7973-7981, 1987
A/Title: Structure and expression of the human apolipoprotein A-IV gene.
A/Reference number: A29330; MUID:87250378; PMID:3036793
A/Accession: A29330
A/Molecule type: DNA
A/Residues: 1-157, 'T', 159, 'Y', 161-278, 'R', 280-326, 'T', 328-379, 'H', 381-396 <EL>
A/Cross-references: GB:J02758; NID:gl78756; PIDN:AAA96733.1; PID:gl78757
R;Elshourbagy, N.A.; Walker, D.W.; Boguski, M.S.; Gordon, J.I.; Taylor, J.M.
J. Biol. Chem. 261, 1998-2002, 1986
A/Title: The nucleotide and derived amino acid sequence of human apolipoprotein A-IV mRNA
A/Reference number: A26280; MUID:86111895; PMID:3080432
A/Accession: A26280
A/Molecule type: mRNA
A/Residues: 21-157, 'T', 159, 'Y', 161-278, 'R', 280-326, 'T', 328-379, 'H', 381-396 <EL2>
A/Cross-references: GB:M14566; NID:gl78778; PIDN:AAA51748.1; PID:gl78779
R;Yang, C.Y.; Gu, Z.W.; Chong, I.S.; Xiong, W.J.; Rosseneu, M.; Yang, H.X.; Lee, B.R.; G
Biochim. Biophys. Acta 1002, 231-237, 1989
A/Title: The primary structure of human apolipoprotein A-IV.
A/Reference number: I37177; MUID:89194198; PMID:2930771
A/Accession: I37177
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-157, 'T', 159, 'Y', 161-278, 'R', 280-396 <YANI>
A/Cross-references: EMBL:X13629; NID:G28761; PIDN:CAA31955.1; PID:G28762
A/Note: submitted to the EMBL Data Library, January 1989
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A/Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A/Reference number: A54223; MUID:94162201; PMID:8117655
A/Accession: C54223
A/Molecule type: protein
A/Residues: 'X', 22, 'X', 24, 'X', 26-31, 'X', 33-34 <KUN>
R;Tenkanen, H.; Lukka, M.; Jauhainen, M.; Metso, J.; Baumann, M.; Peltonen, L.; Ehnholm

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Arterioscler. Thromb. 11, 851-856, 1991
A/Title: The mutation causing the common apolipoprotein A-IV polymorphism is a glutamin
A/Reference number: A61203; MUID:91291788; PMID:2065039
A/Accession: A61203
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 378-379, 'H', 381-382 <TEN>
C/Comment: ApoA-IV is a major lipoprotein of lymph chylomicrons. In human plasma, it is
C/Comment: ApoA-IV is synthesized primarily in the intestine.
C/Genetics:
A/Gene: GDB:APOA4
A/Cross-references: GDB:119000; OMIM:107690
A/Map position: 11q23-11q23
A/Introns: 17/1; 59/2
C/Superfamily: apolipoprotein A-I
C/Keywords: chylomicron; HDL; intestine; lipid binding; lipid transport; lipoprotein; p
F;1-20/Domain: signal sequence #status experimental <SIG>
F;21-396/Product: apolipoprotein A-IV #status experimental <MAT>
Query Match 100.0%; Score 66; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 79 KLVPPFATELHERL 91
|||||
|||||

RESULT 2
A47141
apolipoprotein A-IV I isoform - baboon (fragment)
C/Species: Papio sp. (baboon)
C/Date: 16-Feb-1994 #sequence revision 18-Nov-1994 #text change 12-Apr-1995
C/Accession: A47141
R;Hixson, J.E.; Kammerer, C.M.; Mott, G.E.; Britten, M.L.; Birnbaum, S.; Powers, P.K.;
J. Biol. Chem. 268, 15667-15673, 1993
A/Title: Baboon apolipoprotein A-IV. Identification of Lys76-->Glu that distinguishes t
A/Reference number: A47141; MUID:93340170; PMID:8101842
A/Accession: A47141
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-401 <HIX>
A/Experimental source: intestine
A/Note: sequence extracted from NCBI backbone (NCBI:136009, NCBIP:136010)
C/Superfamily: apolipoprotein A-I
Query Match 100.0%; Score 66; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 63 KLVPPFATELHERL 75
|||||
|||||

RESULT 3
S29565
apolipoprotein A-IV - crab-eating macaque
C/Species: Macaca fascicularis (crab-eating macaque)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C/Accession: S30195; S29565
R;Osada, J.; Pocovi, M.; Nicolosi, R.J.; Schaefer, E.J.; Ordovas, J.M.
Biochim. Biophys. Acta 1172, 335-339, 1993
A/Title: Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III and A-IV
A/Reference number: S30195; MUID:93192330; PMID:8448212
A/Accession: S30195
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-429 <OSA>
A/Cross-references: UNIPROT:P33621; EMBL:X68361; NID:G38050; PIDN:CAA48421.1; PID:G3805
C/Genetics:
A/Introns: 17/1; 59/2
C/Superfamily: apolipoprotein A-I

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Query Match      100.0%; Score 66; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
|||||
Db 79 KLVPPFATELHERL 91

RESULT 4
AG3116
conserved hypothetical protein Atu4555 [imported] - Agrobacterium tumefaciens (strain C58)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 12-Jul-2004
C;Accession: AG3116
R;Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG3116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-261 <KUR>
A;Cross-references: UNIPROT:Q8U799; GB:AE008689; PIDN:AAL45349.1; PID:gl7743042; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4555
A;Map position: linear chromosome
C;Superfamily: conserved hypothetical protein HI1013

Query Match      62.1%; Score 41; DB 2; Length 261;
Best Local Similarity 87.5%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFATELHE 11
|||||
Db 235 PFATEVHE 242

RESULT 5
F98170
hypothetical protein AGR_L_627 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 12-Jul-2004
C;Accession: F98170
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F98170
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <KUR>
A;Cross-references: UNIPROT:Q8U799; GB:AE007870; PIDN:AAK88888.1; PID:gl15158659; GSPDB:C
C;Genetics:
A;Gene: AGR_L_627
A;Map position: linear chromosome
C;Superfamily: conserved hypothetical protein HI1013

Query Match      62.1%; Score 41; DB 2; Length 265;
Best Local Similarity 87.5%; Pred. No. 8.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFATELHE 11
|||||
Db 239 PFATEVHE 246
```

```
RESULT 6
LPB12
apolipoprotein A-I precursor (clone 2Zap AI) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S06064
R;Paraskevopoulou, T.B.; Kritsis, A.; Zannis, V.
submitted to the EMBL Data Library, July 1989
A;Reference number: S06064
A;Accession: S06064
A;Molecule type: mRNA
A;Residues: 1-266 <PAR>
A;Cross-references: UNIPROT:P09809; EMBL:X15908; NID:gl1457; PIDN:CAA34024.1; PID:gl1458
C;Comment: This protein is synthesized in the small intestine.
C;Comment: This protein is a major component of the high density lipoproteins in plasma
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid transport; plasma; tandem rep
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status predicted <PRO>
F;25-266/Product: apolipoprotein A-I #status experimental <MAT>

Query Match      60.6%; Score 40; DB 1; Length 266;
Best Local Similarity 53.8%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
|||||
Db 185 KLVPPFATELHERL 197

RESULT 7
A24998
apolipoprotein A-I - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1993
C;Accession: A24998
R;Yang, C.; Yang, T.; Pownall, H.J.; Gotto Jr., A.M.
Eur. J. Biochem. 160, 427-431, 1986
A;Title: The primary structure of apolipoprotein A-I from rabbit high-density lipoprote
A;Reference number: A24998; MUID:87030294; PMID:3095115
A;Accession: A24998
A;Molecule type: protein
A;Residues: 1-241 <YAN>
C;Superfamily: apolipoprotein A-I
C;Keywords: HDL; lipid binding; lipoprotein

Query Match      59.1%; Score 39; DB 2; Length 241;
Best Local Similarity 53.8%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
|||||
Db 160 KLVPPFATELHERL 172

RESULT 8
S70629
Rad51 homolog mei-3 - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70629
R;Hatakeyama, S.; Ishii, C.; Inoue, H.
Mol. Gen. Genet. 245, 439-446, 1995
A;Title: Identification and expression of the Neurospora crassa mei-3 gene which encode
A;Reference number: S70629; MUID:96133684; PMID:8552049
A;Accession: S70629
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <HAT>
A;Cross-references: UNIPROT:P87210; EMBL:D29638; NID:gl339941; PIDN:BAA20366.1; PID:g21
C;Genetics:
A;Gene: mei-3
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A;Introns: 32/3; 82/1

C;Superfamily: yeast DNA repair protein RAD51

Query Match 59.1%; Score 39; DB 2; Length 353;

Best Local Similarity 56.2%; Pred. No. 27;

Matches 9; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 KLVPPF---ATELHER 12

|||||

84 KLVPMGFTTATEMHQR 99

RESULT 9

E96752

hypothetical protein F28P22.5 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: E96752

R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: E96752

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-697 <STO>

A;Cross-references: UNIPROT:Q9CA19; GB:AE005173; NID:g6648152; PIDN:AAF21152.1; GSPDB:GN

C;Genetics:

A;Gene: F28P22.5

A;Map position: 1

Query Match

Best Local Similarity 61.5%; Score 39; DB 2; Length 697;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13

|||||

647 RLKEFATEDHERI 659

RESULT 10

JC4743

fatty-acid synthase (EC 2.3.1.85) - Mycobacterium bovis

C;Species: Mycobacterium bovis

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C;Accession: JC4743

R;Fernandes, N.D.; Kolattukudy, P.E.

Gene 170, 95-99, 1996

A;Title: Cloning, sequencing and characterization of a fatty acid synthase-encoding gene

A;Reference number: JC4743; MUID:96200863; PMID:8621098

A;Accession: JC4743

A;Molecule type: DNA

A;Residues: 1-2796 <FER>

A;Cross-references: UNIPROT:Q48926; GB:U36763; NID:g1036834; PIDN:AA03809.1; PID:g10368

A;Note: the source is designated as Mycobacterium tuberculosis var. bovis BCG

C;Comment: This enzyme catalyzes both de novo synthesis and chain elongation of fatty ac

C;Genetics:

A;Gene: fas

C;Superfamily: Mycobacterium tuberculosis fatty-acid synthase

F;2188-2193/Region: nucleotide binding #status predicted

F;1693/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

F;2598/Active site: Cys #status predicted

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 2796;

Best Local Similarity 80.0%; Pred. No. 2.5e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13

|||||

Db 2755 PNETELHERL 2764

RESULT 11

H70656

fatty-acid synthase (EC 2.3.1.85) - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C;Accession: H70656

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70656

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-3069 <COL>

A;Cross-references: UNIPROT:P95029; GB:Z83863; GB:AL123456; NID:g3261685; PIDN:CAB06201

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: fas

C;Superfamily: Brevibacterium ammoniagenes fatty-acid synthase

C;Keywords: acyltransferase; coenzyme A

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 3069;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13

|||||

Db 2881 PNETELHERL 2890

RESULT 12

A87058

fatty acid synthase [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: A87058

R;Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A;Title: Massive gene decay in the leprosy bacillus.

A;Reference number: A86909; MUID:21128732; PMID:11234002

A;Accession: A87058

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-3076 <STO>

A;Cross-references: UNIPROT:Q9X7E2; GB:AL450380; NID:gl3093156; PIDN:CAC31572.1; GSPDB:G

C;Genetics:

C;Superfamily: Brevibacterium ammoniagenes fatty-acid synthase

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 3076;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13

|||||

Db 2888 PNETELHERL 2897

RESULT 13

G70313
lipopolysaccharide heptosyltransferase (BC 2.4.99.-) II rfaC2 [similarity] - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70313
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70313
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-317 <AQF>
A;Cross-references: UNIPROT:O6G538; GB:AE000675; PIDN:AAC06484.1; PID:G298
A;Experimental source: strain VF5
C;Genetics:
C;Superfamily: ADP-heptose-LPS heptosyltransferase II
C;Keywords: glycosyltransferase

Query Match 57.6%; Score 38; DB 2; Length 317;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 1 KLVPPFATELHE 11
|||||
Db 110 KLVPHRWELHE 120

RESULT 14
LPRTA4
apolipoprotein A-IV precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C;Accession: A03095; A25214; C24700
R;Boguski, M.S.; Elshourbagy, N.; Taylor, J.M.; Gordon, J.I.
Proc. Natl. Acad. Sci. U.S.A. 81, 5021-5025, 1984
A;Title: Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segment.
A;Reference number: A03095; MUID:84298074; PMID:6591177
A;Accession: A03095
A;Molecule type: mRNA
A;Residues: 1-391 <BOG>
A;Cross-references: UNIPROT:P02651; GB:M00002; GB:K02421; NID:G202949; PIDN:AAA85909.1;
R;Boguski, M.S.; Birkenmeier, E.H.; Elshourbagy, N.A.; Taylor, J.M.; Gordon, J.I.
J. Biol. Chem. 261, 6398-6407, 1986
A;Title: Evolution of the apolipoproteins. Structure of the rat APO-A-IV gene and its re
A;Reference number: A25214; MUID:86196059; PMID:3009456
A;Accession: A25214
A;Molecule type: protein
A;Residues: 1-252, 'Q', 254-391 <BO2>
R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-
A;Reference number: A92558; MUID:87008540; PMID:3020028
A;Accession: C24700
A;Molecule type: DNA
A;Residues: 1-252, 'Q', 254-391 <HAD>
A;Cross-references: GB:J02588; NID:G202937; PIDN:AAA40747.1; PID:G202941
C;Comment: This apoprotein is a major component of HDL and chylomicrons but, unlike other
C;Comment: Nine of the thirteen 22-amino acid tandem repeats (each 22-mer is actually a
cal, and many of these helices are amphipathic. They may therefore serve as lipid-binding
C;Superfamily: apolipoprotein A-I
C;Keywords: chylomicron; duplication; HDL; lipid transport; plasma; tandem repeat
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-391/Product: apolipoprotein A-IV #status predicted <MAT>
F;33-330/Region: 22-residue repeats

Query Match 57.6%; Score 38; DB 1; Length 391;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVPPFATELHER 12

Db 179 MVPFANELKEK 189
|||||
RESULT 15
C75567
adenylosuccinate synthase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: C75567
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Sheth, H.O.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 <WHI>
A;Cross-references: UNIPROT:Q9RYB5; GB:AE001867; GB:AE000513; NID:G6457693; PIDN:AAF096
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0035
A;Map position: 1
C;Superfamily: adenylosuccinate synthase

Query Match 57.6%; Score 38; DB 2; Length 405;
Best Local Similarity 75.0%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFATELHE 11
|||||
Db 266 PFATEVHD 273

RESULT 16
D84153
adenylosuccinate synthetase purA [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D84153
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D84153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <STO>
A;Cross-references: UNIPROT:Q9K5R0; GB:AP001520; GB:BA000004; NID:G10176401; PIDN:BAB07
A;Experimental source: strain C-125
C;Genetics:
A;Gene: purA
C;Superfamily: adenylosuccinate synthase

Query Match 57.6%; Score 38; DB 2; Length 428;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
|||||
Db 276 PFPELHDEI 285

RESULT 17
G97653
adenylosuccinate synthetase (IMP-aspartate ligase) (adas) [imported] - Agrobac
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: G97653
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldmar
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markeiz, B.

Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G97653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <KUR>
A;Cross-references: UNIPROT:Q8UCN6; GB:AE007869; PIDN:AAK88184.1; PID:g15157630; GSPDB:G000000000
C;Genetics:
A;Gene: AGR_C_4442
A;Map position: circular chromosome
C;Superfamily: adenylosuccinate synthase

Query Match 57.6%; Score 38; DB 2; Length 432;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
DB 279 PFPTELHDEI 288

RESULT 18
AE2877
adenylosuccinate synthetase [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2877
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.; E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2877
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <KUR>
A;Cross-references: UNIPROT:Q8UCN6; GB:AE008688; PIDN:AAL43435.1; PID:g17740937; GSPDB:G000000000
C;Genetics:
A;Gene: purA
A;Map position: circular chromosome
C;Superfamily: adenylosuccinate synthase

Query Match 57.6%; Score 38; DB 2; Length 432;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
DB 279 PFPTELHDEI 288

RESULT 19
AD0747
alpha,alpha-trehalose-phosphate synthase (UDP-forming) (EC 2.4.1.15) - *Salmonella enterica* serovar Typhi
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
A;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0747
R;Farhnik, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Typhi
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0747
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-473 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05679.1; PID:g16503174; GSPDB:GN00176
C;Genetics:
A;Gene: STY2137
C;Superfamily: Schizosaccharomyces pombe alpha,alpha-trehalose-phosphate synthase (UDP-forming)
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 57.6%; Score 38; DB 2; Length 473;
Best Local Similarity 63.6%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVFPATELHER 12
DB 133 LLPFASERKR 143

RESULT 20
F69501
acetolactate synthase, large subunit (ilvB-3) homolog - *Archaeoglobus fulgidus*
C;Species: *Archaeoglobus fulgidus*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: F69501
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Pyrococcus furiosus*
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69501
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-543 <KLE>
A;Cross-references: UNIPROT:028264; GB:AE000963; GB:AE000782; MID:g26689286; PIDN:AAB892
C;Superfamily: Acetolactate synthase, large subunit/pyruvate oxidase; thiamin pyrophosphatase

Query Match 57.6%; Score 38; DB 2; Length 543;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVFPATELHE 11
DB 126 RLVPETHRLHE 136

RESULT 21
E71251
probable oligonucleotide hydrolase F - *Syphilis spirochete*
C;Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: E71251
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn, L.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDermott, P.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: E71251
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-589 <COL>
A;Cross-references: UNIPROT:083989; GB:AE001270; GB:AE000520; MID:g33233350; PIDN:AAC659
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP1026

Query Match 57.6%; Score 38; DB 2; Length 589;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VFPATELHER 12
DB 111

Db 246 VPLAELHEQ 255

RESULT 22

RF28 protein - Arabidopsis thaliana retrotransposon (fragment)
T52436
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52436
R;Kawahara, A.; Kato, A.; Komeda, Y.
submitted to the Protein Sequence Database, October 2000
A;Reference number: Z26076
A;Accession: T52436
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-847 <KUW>
A;Cross-references: UNIPROT:Q9SLUA; EMBL:AB028223; PIDN:BA087949.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 1
A;Note: RF28
C;Superfamily: retrovirus-related polyprotein

Query Match 57.6%; Score 38; DB 2; Length 847;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13

Db 159 PTLTEIHERL 168

RESULT 23

JC5047
ras GTPase-activating protein - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5047
R;Kobayashi, M.; Masui, T.; Kusuda, J.; Kameoka, Y.; Hashimoto, K.; Iwashita, S.
Gene 175, 173-177, 1996
A;Title: Human rasGTPase-activating protein (human counterpart of GAP1m): Sequence of the
A;Reference number: JC5047; MUID:97074668; PMID:8917095
A;Accession: JC5047
A;Molecule type: mRNA
A;Residues: 1-850 <KOB>
A;Cross-references: UNIPROT:Q15283; DBJ:D78155; NID:q1060908; PIDN:BA011230.1; PID:d101
C;Comment: This protein plays a role in the regulation of cell growth and differentiation
C;Genetics:
A;Gene: GAP1m
A;Map position: 3q24-26
F;356-568/Domain: ras-specific GAP catalytic domain homology <GAP>
F;603-704/Domain: pleckstrin repeat homology <PK>

Query Match 57.6%; Score 38; DB 2; Length 850;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPFATELHE 11

Db 373 KLVPFATAVAE 383

RESULT 24

AG2381
glycine cleavage system protein P [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AG2381
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchih
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2381

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-983 <KUR>

A;Cross-references: UNIPROT:QBYNE9; GB:BA000019; PIDN:BA076306.1; PID:gl7133744; GSPDB:
A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all4607

Query Match 57.6%; Score 38; DB 2; Length 983;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLVPFATELHERL 13

Db 64 KTVPSAIRLHEQL 76

RESULT 25

TQBS30
transposase - Bacillus thuringiensis transposon Tn430
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S00570; S02241
R;Mahillon, J.; Lereclus, D.
EMBO J. 7, 1515-1526, 1988
A;Title: Structural and functional analysis of Tn430: identification of an integrase-1
A;Reference number: S00554; MUID:88312602; PMID:2842151
A;Accession: S00570
A;Molecule type: DNA
A;Residues: 1-987 <MAH1>
A;Cross-references: UNIPROT:P10021; EMBL:X07651; NID:G40347; PIDN:CAA30492.1; PID:G4034
R;Mahillon, J.; Seurinck, J.
Nucleic Acids Res. 16, 11827-11828, 1988
A;Title: Complete nucleotide sequence of pGI2, a Bacillus thuringiensis plasmid contain
A;Reference number: S02047; MUID:89098342; PMID:3211758
A;Accession: S02241
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-987 <MAH2>
A;Cross-references: EMBL:X13481; NID:G3171732; PIDN:CAA31833.1; PID:G40318
C;Genetics:

A;Gene: tnpA

C;Superfamily: transposase Tn21

C;Keywords: DNA binding; DNA replication

Query Match 57.6%; Score 38; DB 1; Length 987;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVPFATELHERL 13

Db 288 LIDYATIEHDRL 299

RESULT 26

TQ1397
LTR gag/pol polyprotein homolog T419.16 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01397
R;Parnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.; Schutz, K.; Hu
submitted to the EMBL Data Library, May 1998
A;Description: Genomic sequence of BAC T419 from Arabidopsis thaliana, chromosome IV, n
A;Reference number: Z14314
A;Accession: T01397
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1456 <PAR>
A;Cross-references: UNIPROT:Q9T94; EMBL:AF069442; NID:G3242970; PID:G3924609
A;Experimental source: cultivar Columbia
C;Genetics:

RESULT 27

TQ1397
LTR gag/pol polyprotein homolog T419.16 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01397
R;Parnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.; Schutz, K.; Hu
submitted to the EMBL Data Library, May 1998
A;Description: Genomic sequence of BAC T419 from Arabidopsis thaliana, chromosome IV, n
A;Reference number: Z14314
A;Accession: T01397
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1456 <PAR>
A;Cross-references: UNIPROT:Q9T94; EMBL:AF069442; NID:G3242970; PID:G3924609
A;Experimental source: cultivar Columbia
C;Genetics:

```

A;Map position: 4
A;Introns: 129/1
A;Note: T419.16
C;Superfamily: retrovirus-related polyprotein

Query Match      57.6%; Score 38; DB 2; Length 1456;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 PFATELHERL 13
      |||:||||
Db      175 PSITEIHERL 184

RESULT 27
B85188
retrotransposon like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85188
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85188
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1474 <STO>
A;Cross-references: UNIPROT:O23529; GB:NC_001268; NID:G5302802; PIDN:CAB46043.1; GSPDB:G
C;Genetics:
A;Map position: 4
A;Gene: dl4465c
C;Superfamily: retrovirus-related polyprotein

Query Match      57.6%; Score 38; DB 2; Length 1474;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 PFATELHERL 13
      |||:||||
Db      202 PSITEIHERL 211

RESULT 28
E71436
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: E71436
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; And
C.; Chalwatzi, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: E71436
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2088 <BEV>
A;Cross-references: UNIPROT:O23529; GB:297342; NID:G2245031; PID:G2245044
C;Genetics:
A;Map position: 4COP9-4C3845

Query Match      57.6%; Score 38; DB 2; Length 2088;
Best Local Similarity 70.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 PFATELHERL 13
      |||:||||

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Db      886 PSITEIHERL 895

RESULT 29
T26500
peptidylprolyl isomerase (EC 5.2.1.8) Y17G7B.9 [similarity] - Caenorhabditis elegans
N;Contains: cyclophilin
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26500
R;Smye, R.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20225
A;Accession: T26500
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-222 <WIL>
A;Cross-references: UNIPROT:Q9XX17; EMBL:AL023828; PIDN:CAAL19454.1; GSPDB:GN000020; CESP
A;Experimental source: clone Y17G7B
C;Genetics:
A;Gene: CESP:Y17G7B.9
A;Map position: 2
A;Introns: 14/3; 60/1; 84/3
C;Superfamily: peptidylprolyl isomerase; cyclophilin homology
C;Keywords: cis-trans-isomerase

Query Match      56.1%; Score 37; DB 2; Length 222;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 PFATELHERL 13
      |||:||||
Db      82 PFKDEIHOQL 91

RESULT 30
JQ0704
apolipoprotein A-I - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Oct-1994
C;Accession: JQ0704
R;Weiler-Guettler, H.; Sommerfeldt, M.; Papandrikopoulou, A.; Mischek, U.; Bonitz, D.; J.
Neurochem. 54, 444-450, 1990
A;Title: Synthesis of apolipoprotein A-I in pig brain microvascular endothelial cells.
A;Reference number: JQ0704; MUID:90132667; PMID:2105375
A;Accession: JQ0704
A;Molecule type: mRNA
A;Residues: 1-231 <WEI>
A;Note: the authors translated the codon CAG for residue 124 as His and GAC for residue
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; lipid binding; lipid transport; lipoprotein; p

Query Match      56.1%; Score 37; DB 2; Length 231;
Best Local Similarity 61.5%; Pred. No. 40;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 KLVPPFATELHERL 13
      |||:||||
Db      129 KLSPLAEELRDRL 141

RESULT 31
A24700
apolipoprotein A-I precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A24700; S00298; A05314
R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.
J. Biol. Chem. 261, 13268-13277, 1986
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A
A;Reference number: A92558; MUID:87008540; PMID:3020028
A;Accession: A24700
A;Molecule type: DNA

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A;Residues: 1-259 <HAD>
A;Cross-references: UNIPROT:P04639; EMBL:J02597; NID:g202935; PIDN:AAA40745.1; PID:g202949
R;Poncin, J.E.; Martial, J.A.; Gielen, J.E.
Eur. J. Biochem. 140, 493-498, 1984
A;Title: Cloning and structure analysis of the rat apolipoprotein A-I cDNA.
A;Reference number: S00298; MUID:84207987; PMID:6426956
A;Accession: S00298
A;Molecule type: mRNA
A;Residues: 1-259 <PON>
A;Cross-references: GB:M00001; EMBL:X00558; NID:g202944; PIDN:AAA40749.1; PID:g202945
R;Gordon, J.I.; Smith, D.P.; Andy, R.; Alpers, D.H.; Schonfeld, G.; Straus, A.W.
J. Biol. Chem. 257, 971-978, 1982
A;Title: The primary translation product of rat intestinal apolipoprotein A-I mRNA is an
A;Reference number: A05314; MUID:82098162; PMID:6798036
A;Accession: A05314
A;Molecule type: protein
A;Residues: 1-18, 'X', 20-21, 'X', 23-28, 'X', 30-38, 'X', 40-41, 'X', 43-45 <GOR>
C;Comment: This protein is synthesized in the liver and small intestine. The propeptide
C;Comment: This protein is a major component of the high density lipoproteins in plasma.
C;Genetics:
A;Introns: 15/1; 66/2
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid transport; lipid
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-259/Product: apolipoprotein A-I #status experimental <WAT>
Query Match 56.1%; Score 37; DB 2; Length 259;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLVPFATLH 11
DB 141 KLSPLGLTGLH 151
RESULT 32
S31394
apolipoprotein A-I - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31394
R;Moechel, B.; Flach, R.; Weiss, B.; Weiler-Guettiler, H.; Frey, A.; Zinke, H.; Gassen, H.
submitted to the EMBL Data Library, November 1992
A;Description: Genomic organization of the porcine apolipoprotein A1 gene and study of
A;Reference number: S31394
A;Accession: S31394
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-264 <MOE>
A;Cross-references: UNIPROT:P18648; EMBL:X69477; NID:g1889; PIDN:CAA49234.1; PID:g1890
C;Superfamily: apolipoprotein A-I
Query Match 56.1%; Score 37; DB 2; Length 264;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KLVPFATLH 13
DB 162 KLSPLAEELRDL 174
RESULT 33
A46018
apolipoprotein AI - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46018
R;Birchbauer, A.; Knipping, G.; Juritsch, B.; Aechauer, H.; Zechner, R.
Genomics 15, 643-652, 1993
A;Title: Characterization of the apolipoprotein AI and CIII genes in the domestic pig.
A;Reference number: A46018; MUID:93224154; PMID:8468059
A;Accession: A46018

A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-265 <BIR>
A;Cross-references: UNIPROT:P18648; GB:L00626; NID:g164358; PIDN:AAA30992.1; PID:g16435
C;Note: sequence extracted from NCBI backbone (NCBIN:129509, NCBI:P:129511)
C;Superfamily: apolipoprotein A-I
Query Match 56.1%; Score 37; DB 2; Length 265;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLVPFATLH 13
DB 163 KLSPLAEELRDL 175
RESULT 34
JT0672
apolipoprotein A-I - pig
N;Alternate names: apo-A-I
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: JT0672; PN0471; A05311
R;Fried, V.N.; Patel, B.; Zhan, R.; Black, D.D.
Gene 134, 267-270, 1993
A;Title: Sequence of the porcine apoA-I gene.
A;Reference number: JT0672; MUID:94085789; PMID:7916724
A;Accession: JT0672
A;Molecule type: DNA
A;Residues: 1-265 <TRI>
A;Cross-references: UNIPROT:P18648; EMBL:Z14124; NID:g1893
A;Note: this translation is not annotated in GenBank entry SSAPOAIG, release 111.0; the
R;Fried, V.N.; Hasler-Rapacz, J.; Rapacz, J.; Black, D.D.
Gene 123, 173-179, 1993
A;Title: Sequences and expression of the porcine apolipoprotein A-I and C-III mRNAs.
A;Reference number: PN0471; MUID:93154581; PMID:8428656
A;Accession: PN0471
A;Molecule type: mRNA
A;Residues: 105-265 <TR2>
A;Experimental source: liver
R;Mahley, R.W.; Weisgraber, K.H.; Innerarity, T.; Brewer Jr., H.B.
Biochemistry 15, 1928-1933, 1976
A;Title: Characterization of the plasma lipoproteins and apoproteins of the Erythrocebu
A;Reference number: A90395; MUID:76184721; PMID:178359
A;Accession: A05311
A;Molecule type: protein
A;Residues: 25-34 <MAH>
C;Comment: This protein is the major apolipoprotein of high-density lipoprotein and sei
C;Genetics:
A;Gene: apoA-I
A;Introns: 15/1; 66/2
C;Superfamily: apolipoprotein A-I
C;Keywords: cholesterol metabolism; HDL; intestine; lipid binding; lipid metabolism; li
F;95/Region: ochre stop codon
Query Match 56.1%; Score 37; DB 2; Length 265;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 KLVPFATLH 13
DB 163 KLSPLAEELRDL 175
RESULT 35
C96752
probable DNA-binding protein P28P22.7 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96752
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C: A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96752
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <STO>
A:Cross-references: UNIPROT:Q9CA18; GB:AE005173; NID:g6648154; PIDN:AAF21154.1; GSPDB:GN
C:Genetics:
A:Gene: F28P22.7
A:Map position: 1

Query Match 56.1%; Score 37; DB 2; Length 289;
Best Local Similarity 63.6%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPPFATELHE 11
||: |||: ||
Db 266 KLVVIAEMHE 276

RESULT 36
S35642
RAD51 protein homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S35642
R:Bezzubova, O.; Shinohara, A.; Mueller, R.G.; Ogawa, H.; Buerstedde, J.M.
Nucleic Acids Res. 21, 1577-1580, 1993
A:Title: A chicken RAD51 homologue is expressed at high levels in lymphoid and reproduct
A:Reference number: S35642; MUID:93241937; PMID:8479908
A:Accession: S35642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <BEZ>
A:Cross-references: UNIPROT:P37383; GB:S59426; GB:D09655; NID:g299818; PIDN:AAB26354.1;
C:Superfamily: yeast DNA repair protein RAD51
C:Keywords: DNA binding

Query Match 56.1%; Score 37; DB 2; Length 339;
Best Local Similarity 56.2%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPPF----ATELHER 12
||||| |||: ||
Db 80 KLVPMGFTTATEFHQR 95

RESULT 37
I58295
RAD51 protein homolog - human
N:Alternate names: recombination protein recA homolog
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I58295; S36161; S37673; S35632
R:Yoshimura, Y.; Morita, T.; Yamamoto, A.; Matsushiro, A.
Nucleic Acids Res. 21, 1665, 1993
A:Title: Cloning and sequence of the human RecA-like gene cDNA.
A:Reference number: I58295; MUID:93241950; PMID:8479919
A:Accession: I58295
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBU
A:Molecule type: mRNA
A:Residues: 1-339 <RES>
A:Cross-references: UNIPROT:Q06609; GB:D14134; NID:g285976; PIDN:BAA03189.1; PID:g285977
R:Shinohara, A.; Ogawa, H.; Matsuda, Y.; Ushio, N.; Ikeo, K.; Ogawa, T.
Nature Genet. 4, 239-243, 1993
A:Title: Cloning of human, mouse and fission yeast recombination genes homologous to RAD
A:Reference number: S36159; MUID:93364417; PMID:8358431

A:Accession: S36161
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <SHI>
R:Shinohara, A.; Ogawa, H.; Matsuda, Y.; Ushio, N.; Ikeo, K.; Ogawa, T.
submitted to the EMBL Data Library, December 1992
A:Reference number: S37672
A:Accession: S37673
A:Molecule type: mRNA
A:Residues: 1-312,'Q' 314-339 <SH2>
A:Cross-references: GB:D13804; NID:g397826; PIDN:BAA02962.1; PID:g397827
C:Genetics:
A:Gene: GDB:RECA
A:Cross-references: GDB:138758; OMIM:179617
A:Map position: 15q15.1-15q15.1
C:Superfamily: yeast DNA repair protein RAD51
C:Keywords: DNA recombination; DNA repair; nucleotide binding; P-loop
F;127-134/Region: nucleotide-binding motif A (P-loop)
F;218-222/Region: nucleotide-binding motif B

Query Match 56.1%; Score 37; DB 2; Length 339;
Best Local Similarity 56.2%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPPF----ATELHER 12
||||| |||: ||
Db 80 KLVPMGFTTATEFHQR 95

RESULT 38
A48221
RAD51 protein homolog - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48221; S36160
R:Morita, T.; Yoshimura, Y.; Yamamoto, A.; Murata, K.; Mori, M.; Yamamoto, H.; Matsushiro,
Proc. Natl. Acad. Sci. U.S.A. 90, 6577-6580, 1993
A:Title: A mouse homolog of the Escherichia coli recA and Saccharomyces cerevisiae RAD5
A:Reference number: A48221; MUID:93342035; PMID:8341671
A:Accession: A48221
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-339 <MOR>
A:Cross-references: UNIPROT:Q08297; GB:D13473; NID:g407348; PIDN:BAA02718.1; PID:g40734
A:Experimental source: 129/Sv, testes
A:Note: sequence extracted from NCBI backbone (NCBIN:135814, NCBIP:135815)
R:Shinohara, A.; Ogawa, H.; Matsuda, Y.; Ushio, N.; Ikeo, K.; Ogawa, T.
Nature Genet. 4, 239-243, 1993
A:Title: Cloning of human, mouse and fission yeast recombination genes homologous to RA
A:Reference number: S36159; MUID:93364417; PMID:8358431
A:Accession: S36160
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-339 <SHI>
A:Cross-references: EMBL:D13803; NID:g303702; PIDN:BAA02961.1; PID:g397831
C:Superfamily: yeast DNA repair protein RAD51
C:Keywords: DNA binding

Query Match 56.1%; Score 37; DB 2; Length 339;
Best Local Similarity 56.2%; Pred. No. 60;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 1 KLVPPF----ATELHER 12
||||| |||: ||
Db 80 KLVPMGFTTATEFHQR 95

RESULT 39
S45881
probable purine nucleotide-binding protein YBR025c - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR0309
C:Species: Saccharomyces cerevisiae
C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: S45881; S46556
R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45875
A;Accession: S45881
A;Molecule type: DNA
A;Residues: 1-394 <GRI>
A;Cross-references: UNIPROT:P38219; EMBL:Z35894; NID:G536233; PIDN:CAA84967.1; PID:G536233
A;Experimental source: strain S288C
R;Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A;Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II from *Schizosaccharomyces pombe* ly identified genes and a homologue of the SCO1 gene.
A;Reference number: S46551; MUID:94378725; PMID:8091864
A;Accession: S46556
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-394 <SMI>
A;Cross-references: EMBL:X76078; NID:G498748; PIDN:CAA53682.1; PID:G498754
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Cross-references: SGD:S0000229
A;Map position: 2R
C;Superfamily: yeast probable purine nucleotide-binding protein YBR025c
C;Keywords: Atp; P-loop; purine nucleotide binding
F;27-34/Region: nucleotide-binding motif A (P-loop)
F;33/Binding site: ATP/GTP (Lys) #status predicted

Query Match 56.1%; Score 37; DB 2; Length 394;
Best Local Similarity 50.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LVFPATELHERL 13
: : : : :
Db 262 IIPFVSLEERL 273

RESULT 40
C83347
probable dipeptidase precursor PA2393 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83347
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83347
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-448 <STO>
A;Cross-references: UNIPROT:Q91187; GB:AE004665; GB:AE004091; NID:G9948426; PIDN:AAG0578
A;Experimental source: strain PA01
C;Genetics:
C;Superfamily: membrane dipeptidase

Query Match 56.1%; Score 37; DB 2; Length 448;
Best Local Similarity 53.8%; Pred. No. 81;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLVFPATELHERL 13
: : : : :
Db 41 KVMKHAELHERI 53

RESULT 41
T39621
peptidyl prolyl cis trans isomerase - fission yeast (*Schizosaccharomyces pombe*)
C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39621
R;Wood, V.; Rajandream, M.A.; Barrrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21843
A;Accession: T39621
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: DNA
A;Residues: 1-463 <WOO>
A;Cross-references: UNIPROT:O42941; EMBL:AL022104; PIDN:CAA17903.1; GSPDB:GN00067; SPDB:SPDB:GN00067
A;Experimental source: strain 972h-; cosmid c16H5
C;Genetics:
A;Gene: SPDB:SPBC16H5.05c
A;Map position: 2
A;Introns: 2/3; 12/2; 47/2

Query Match 56.1%; Score 37; DB 2; Length 463;
Best Local Similarity 70.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 PFATELHERL 13
: : : : :
Db 82 PFAVETHRL 91

RESULT 42
S37664
peplomer polyprotein precursor - avian infectious bronchitis virus (strain D1466) (fr
N;Contains: E2 glycoprotein subunit S2
C;Species: avian infectious bronchitis virus, IBV
A;Variety: strain D1466
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S37664
R;Kusters, J.G.; Jager, E.J.; Niesters, H.G.M.; van der Zeijst, B.A.M.
Vaccine 8, 605-608, 1990
A;Title: Sequence evidence for RNA recombination in field isolates of avian coronavirus
A;Reference number: S37663; MUID:91205880; PMID:1708184
A;Accession: S37664
A;Molecule type: genomic RNA
A;Residues: 1-621 <KUS>
A;Cross-references: UNIPROT:Q66196; EMBL:X58001; NID:G58986; PIDN:CAA41065.1; PID:G58986
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; peplomer protein; spike protein
F;1-5/Product: E2 glycoprotein subunit S1 (fragment) #status predicted <GSI>
F;6-621/Product: E2 glycoprotein subunit S2 #status predicted <GS2>
F;10,47,59,137,144,415,447,482,506,519,542/Binding site: carbohydrate (Asn) (covalent)

Query Match 56.1%; Score 37; DB 2; Length 621;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VPATELHERL 13
: : : : :
Db 237 IFFATQLQARI 247

RESULT 43
JC4510
pullulanase (EC 3.2.1.41) precursor - yeast (*Lipomyces kononenkoae*)
N;Alternate names: LKA1 protein; raw starch-degrading amylase
N;Contains: alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)
C;Species: Lipomyces kononenkoae
C;Date: 07-Feb-1996 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4510; PC4116
R;Steyn, A.J.C.; Marmur, J.; Pretorius, I.S.
Gene 166, 65-71, 1995
A;Title: Cloning, sequence analysis and expression in yeasts of a cDNA containing a Lip
A;Reference number: JC4510; MUID:96105202; PMID:8529895
A;Accession: JC4510
A;Molecule type: mRNA
A;Residues: 1-624 <STE>
A;Cross-references: UNIPROT:Q01117; GB:U30376; NID:g1173536; PIDN:AAC49622.1; PID:g1173536
A;Experimental source: strain IGC4052B

A;Accession: PC4116
A;Molecule type: protein
A;Residues: 29-44 <ST2>
A;Experimental source: IGC4052B
C;Genetics:
A;Gene: LKA1
C;Function:

A;Description: hydrolyzes raw starch, degrading both alpha-1,4 and alpha-1,6 linkages
A;Pathway: glycogen/starch degradation
C;Superfamily: Lipomycetes alpha-amylase; alpha-amylase core homology; glucoamylase starch
C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-624/Product: alpha-amylase #status predicted <MAT>
F;48-141/Domain: glucoamylase starch-binding domain homology <SBD>
F;320-447/Domain: alpha-amylase core homology <AMY>
F;177-185,297-311,367-430,587-622/Disulfide bonds: #status predicted
F;304,344/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;357,377,444/Active site: His, Glu, Asp #status predicted

Query Match 56.1%; Score 37; DB 1; Length 624;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LVFPATELHER 12
: : ||||| :
Db 247. LIALATELHNR 257

RESULT 44

S37663
peplomeric polyprotein precursor - avian infectious bronchitis virus (strain D207) (frag
N;Contains: E2 glycoprotein subunit S2
C;Species: avian infectious bronchitis virus, IBV
A;Variety: strain D207
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S37663
R;Kusters, J.G.; Jager, E.J.; Niesters, H.G.M.; van der Zeijst, B.A.M.
Vaccine 8, 605-608, 1990
A;Title: Sequence evidence for RNA recombination in field isolates of avian coronavirus
A;Reference number: S37663; MUID:91205880; PMID:1708184
A;Accession: S37663
A;Molecule type: genomic RNA
A;Residues: 1-630 <KUS>

A;Cross-references: UNIPROT:Q66197; EMBL:X58003; NID:958988; PIDN:CAA41067.1; PID:958989
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; peplomer protein; spike protein
F;1-5/Product: E2 glycoprotein subunit S1 (fragment) #status predicted <GS1>
F;6-621/Product: E2 glycoprotein subunit S2 #status predicted <GS2>
F;10,47,59,137,144,415,447,482,506,519,542/Binding site: carbohydrate (Asn) (covalent) #

Query Match 56.1%; Score 37; DB 2; Length 630;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 VFPATELHERL 13
: ||||| :
Db 237 IPFATQLQARI 247

RESULT 45

S39630
multidrug-efflux transport protein B - Pseudomonas aeruginosa
N;Alternate names: multidrug resistance protein B
C;Species: Pseudomonas aeruginosa
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S39630
R;Poole, K.; Heinrichs, D.E.; Neshat, S.
Mol. Microbiol. 10, 529-544, 1993
A;Title: Cloning and sequence analysis of an EnvCD homologue in Pseudomonas aeruginosa:
A;Reference number: S39629; MUID:95058196; PMID:7968531
A;Accession: S39630
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1046 <POO>
A;Cross-references: UNIPROT:P52002; GB:L11616; NID:9438852; PIDN:AAA74437.1; PID:943885
A;Experimental source: strain CD10
C;Genetics:
A;Gene: mexB
C;Function:

A;Description: probably involved in secretion of the siderophore pyoverdine
A;Note: inducible under conditions of iron limitation
C;Superfamily: acriflavin resistance protein
C;Keywords: transmembrane protein; transport protein
F;14-30/Domain: transmembrane #status predicted <TM1>
F;343-359/Domain: transmembrane #status predicted <TM2>
F;370-386/Domain: transmembrane #status predicted <TM3>
F;397-413/Domain: transmembrane #status predicted <TM4>
F;442-458/Domain: transmembrane #status predicted <TM5>
F;472-488/Domain: transmembrane #status predicted <TM6>
F;541-557/Domain: transmembrane #status predicted <TM7>
F;874-890/Domain: transmembrane #status predicted <TM8>
F;898-914/Domain: transmembrane #status predicted <TM9>
F;973-989/Domain: transmembrane #status predicted <TM10>
F;1014-1030/Domain: transmembrane #status predicted <TM11>

Query Match 56.1%; Score 37; DB 2; Length 1046;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVFPATELHER 12
: : ||||| :
Db 944 IVEFAKELHEQ 954

Search completed: September 1, 2005, 16:41:28
Job time : 42 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 16:35:05 ; Search time 162 Seconds
(without alignments)
31.603 Million call updates/sec

Title: US-09-993-366-1

Perfect score: 66

Sequence: 1 KLVPPATELHERL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1774312 seqs, 393823214 residues

Total number of hits satisfying chosen parameters: 1774312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

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1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	66	100.0	13	10	US-09-991-809-2
2	66	100.0	85	18	US-10-731-875A-46
3	66	100.0	85	18	US-10-731-875A-47
4	66	100.0	85	18	US-10-731-875A-48
5	66	100.0	85	18	US-10-731-875A-49
6	66	100.0	382	9	US-09-800-729-206
7	66	100.0	382	9	US-09-987-107-37
8	66	100.0	382	18	US-10-987-454-28
9	66	100.0	382	19	US-11-017-037-37
10	66	100.0	382	20	US-11-017-059-37
11	66	100.0	396	9	US-09-800-729-207

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66	100.0	396	10	US-09-802-640-16	Sequence 16, Appl
66	100.0	396	15	US-10-403-902A-16	Sequence 16, Appl
66	100.0	396	17	US-10-741-600-1631	Sequence 1631, Ap
66	100.0	396	17	US-10-741-600-1632	Sequence 1632, Ap
66	100.0	396	18	US-10-987-454-7	Sequence 7, Appl
66	100.0	396	19	US-11-017-037-33	Sequence 33, Appl
66	100.0	396	20	US-11-017-059-33	Sequence 36, Appl
66	100.0	401	9	US-09-987-107-36	Sequence 36, Appl
66	100.0	401	18	US-10-987-454-29	Sequence 29, Appl
66	100.0	401	18	US-10-987-454-32	Sequence 32, Appl
66	100.0	401	19	US-11-017-037-35	Sequence 36, Appl
66	100.0	401	20	US-11-017-059-36	Sequence 36, Appl
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49	59.1	397	15	US-10-369-493-3721	Sequence 3721, Ap
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51	59.1	2796	9	US-09-870-759-114	Sequence 114, App
52	59.1	2796	10	US-09-751-708A-114	Sequence 114, App
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54	59.1	2796	16	US-10-742-350-31	Sequence 31, Appl
55	59.1	2796	16	US-10-428-817A-110	Sequence 110, App
56	59.1	2796	17	US-10-937-758A-91	Sequence 91, Appl
57	59.1	3069	9	US-09-712-363-246	Sequence 246, App
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71	57.6	314	15	US-10-440-503-10	Sequence 10, Appl
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76	57.6	391	14	US-10-316-253-242	Sequence 242, App
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82	57.6	405	15	US-10-369-493-14854	Sequence 14854, A
83	57.6	405	15	US-10-369-493-15043	Sequence 15043, A
84	57.6	405	15	US-10-369-493-23391	Sequence 23391, A

85 38 57.6 428 15 US-10-369-493-17483 Sequence 17483, A
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 87 38 57.6 429 15 US-10-282-122A-45455 Sequence 45455, A
 88 38 57.6 473 15 US-10-389-566-1358 Sequence 1358, Ap
 89 38 57.6 516 15 US-10-425-114-63544 Sequence 63544, A
 90 38 57.6 542 16 US-10-425-115-331388 Sequence 331388,
 91 38 57.6 652 14 US-10-156-761-12996 Sequence 12996, A
 92 38 57.6 669 17 US-10-892-544-2 Sequence 2, Appli
 93 37 56.1 107 18 US-10-731-875A-38 Sequence 38, Appl
 94 37 56.1 107 18 US-10-731-875A-39 Sequence 39, Appl
 95 37 56.1 124 16 US-10-425-115-244210 Sequence 244210,
 96 37 56.1 166 15 US-10-389-674-44 Sequence 44, Appl
 97 37 56.1 166 15 US-10-389-674-56 Sequence 56, Appl
 98 37 56.1 166 15 US-10-389-674-65 Sequence 65, Appl
 99 37 56.1 170 16 US-10-437-963-155938 Sequence 155938,
 100 37 56.1 239 18 US-10-987-454-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
 US-09-991-809-2
 ; Sequence 2, Application US/09991809
 ; Publication No. US20030100014A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jackowski, George
 ; TITLE OF INVENTION: Apolipoprotein Biopolymer Markers Predictive of Type II Diabetes
 ; FILE REFERENCE: 2132.111
 ; CURRENT APPLICATION NUMBER: US/09/991,809
 ; CURRENT FILING DATE: 2001-11-23
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-991-809-2

Query Match 100.0%; Score 66; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 Db 1 KLVPPFATELHERL 13

RESULT 2
 US-10-731-875A-46
 ; Sequence 46, Application US/10731875A
 ; Publication No. US20050149269A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Applera Corporation
 ; APPLICANT: Thomas, Paul
 ; APPLICANT: Kejariwal, Anish
 ; APPLICANT: Campbell, Michael
 ; APPLICANT: Mi, Huaiyu
 ; APPLICANT: Diemer, Karen
 ; APPLICANT: Guo, Nan
 ; APPLICANT: Ladunga, Istvan
 ; APPLICANT: Lazareva, Betty
 ; APPLICANT: Muruganujan, Anushya
 ; APPLICANT: Rabkin, Steven
 ; APPLICANT: Vandergriff, Jody
 ; TITLE OF INVENTION: Browseable Database For Biological Use
 ; FILE REFERENCE: 9692-000029
 ; CURRENT APPLICATION NUMBER: US/10/731,875A
 ; CURRENT FILING DATE: 2003-12-09
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 46

; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary Protein Sequence.
 US-10-731-875A-46

Query Match 100.0%; Score 66; DB 18; Length 85;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 Db 28 KLVPPFATELHERL 40

RESULT 3
 US-10-731-875A-47
 ; Sequence 47, Application US/10731875A
 ; Publication No. US20050149269A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Applera Corporation
 ; APPLICANT: Thomas, Paul
 ; APPLICANT: Kejariwal, Anish
 ; APPLICANT: Campbell, Michael
 ; APPLICANT: Mi, Huaiyu
 ; APPLICANT: Diemer, Karen
 ; APPLICANT: Guo, Nan
 ; APPLICANT: Ladunga, Istvan
 ; APPLICANT: Lazareva, Betty
 ; APPLICANT: Muruganujan, Anushya
 ; APPLICANT: Rabkin, Steven
 ; APPLICANT: Vandergriff, Jody
 ; APPLICANT: Doremieux, Olivier
 ; TITLE OF INVENTION: Browseable Database For Biological Use
 ; FILE REFERENCE: 9692-000029
 ; CURRENT APPLICATION NUMBER: US/10/731,875A
 ; CURRENT FILING DATE: 2003-12-09
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 47
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Unknown
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary Protein Sequence.
 US-10-731-875A-47

Query Match 100.0%; Score 66; DB 18; Length 85;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 Db 28 KLVPPFATELHERL 40

RESULT 4
 US-10-731-875A-48
 ; Sequence 48, Application US/10731875A
 ; Publication No. US20050149269A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Applera Corporation
 ; APPLICANT: Thomas, Paul
 ; APPLICANT: Kejariwal, Anish
 ; APPLICANT: Campbell, Michael
 ; APPLICANT: Mi, Huaiyu
 ; APPLICANT: Diemer, Karen
 ; APPLICANT: Guo, Nan
 ; APPLICANT: Ladunga, Istvan
 ; APPLICANT: Lazareva, Betty
 ; APPLICANT: Muruganujan, Anushya
 ; APPLICANT: Rabkin, Steven

; APPLICANT: Vandergriff, Jody
; APPLICANT: Doremieux, Olivier
; TITLE OF INVENTION: Browseable Database For Biological Use
; FILE REFERENCE: 9692-000029
; CURRENT APPLICATION NUMBER: US/10/731,875A
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 63
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; SEQ ID NO 48
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exemplary Protein Sequence.
US-10-731-875A-48

Query Match 100.0%; Score 66; DB 18; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
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Db 28 KLVPPFATLHERL 40

RESULT 5
US-10-731-875A-49
; Sequence 49, Application US/10731875A
; Publication No. US20050149269A1
; GENERAL INFORMATION:
; APPLICANT: Applera Corporation
; APPLICANT: Thomas, Paul
; APPLICANT: Kejariwal, Anish
; APPLICANT: Campbell, Michael
; APPLICANT: Mi, Huaiyu
; APPLICANT: Diemer, Karen
; APPLICANT: Guo, Nan
; APPLICANT: Ladunga, Istvan
; APPLICANT: Lazareva, Betty
; APPLICANT: Muruganujan, Anushya
; APPLICANT: Rabkin, Steven
; APPLICANT: Vandergriff, Jody
; APPLICANT: Doremieux, Olivier
; TITLE OF INVENTION: Browseable Database For Biological Use
; FILE REFERENCE: 9692-000029
; CURRENT APPLICATION NUMBER: US/10/731,875A
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exemplary Protein Sequence.
US-10-731-875A-49

Query Match 100.0%; Score 66; DB 18; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
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Db 28 KLVPPFATLHERL 40

RESULT 6
US-09-800-729-206
; Sequence 206, Application US/09800729
; Patent No. US20020068319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins

; FILE REFERENCE: P2044PI
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-206

Query Match 100.0%; Score 66; DB 9; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 79 KLVPPFATLHERL 91

RESULT 7
US-09-987-107-37
; Sequence 37, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-987-107-37

Query Match 100.0%; Score 66; DB 9; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
| | | | | | | | | | | | | | | | | | | | | |
Db 79 KLVPPFATLHERL 91

RESULT 8
US-10-987-454-28
; Sequence 28, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733

; PRIOR FILING DATE: 2004-06-16
 ; NUMBER OF SEQ ID NOS: 251
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 28
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-10-987-454-28

Query Match 100.0%; Score 66; DB 18; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
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 Db 79 KLVPPFATLHERL 91

RESULT 9
 US-11-017-037-37
 ; Sequence 37, Application US/11017037
 ; Publication No. US20050096277A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSEN1A
 ; CURRENT APPLICATION NUMBER: US/11/017,037
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: US/09/987,107
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-11-017-037-37

Query Match 100.0%; Score 66; DB 19; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
 |||||
 Db 79 KLVPPFATLHERL 91

RESULT 10
 US-11-017-059-37
 ; Sequence 37, Application US/11017059
 ; Publication No. US20050142639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSEN1A
 ; CURRENT APPLICATION NUMBER: US/11/017,059
 ; CURRENT FILING DATE: 2004-12-21
 ; PRIOR APPLICATION NUMBER: US/09/987,107
 ; PRIOR FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10

; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37
 ; LENGTH: 382
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-11-017-059-37

Query Match 100.0%; Score 66; DB 20; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
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 Db 79 KLVPPFATLHERL 91

RESULT 11
 US-09-800-729-207
 ; Sequence 207, Application US/09800729
 ; Patent No. US20020068319A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: 32 Human secreted proteins
 ; FILE REFERENCE: PZ044P1
 ; CURRENT APPLICATION NUMBER: US/09/800,729
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/26013
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/155,709
 ; PRIOR FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 217
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 207
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-800-729-207

Query Match 100.0%; Score 66; DB 9; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
 |||||
 Db 79 KLVPPFATLHERL 91

RESULT 12
 US-09-987-107-33
 ; Sequence 33, Application US/09987107
 ; Patent No. US20020156007A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GRAVERSEN, Jonas
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
 ; FILE REFERENCE: GRAVERSEN1A
 ; CURRENT APPLICATION NUMBER: US/09/987,107
 ; CURRENT FILING DATE: 2001-11-13
 ; PRIOR APPLICATION NUMBER: US 60/264,022
 ; PRIOR FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057
 ; PRIOR FILING DATE: 2001-01-15
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682
 ; PRIOR FILING DATE: 2000-11-10
 ; NUMBER OF SEQ ID NOS: 91
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-987-107-33

Query Match 100.0%; Score 66; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 13

US-09-802-640-16
Sequence 16, Application US/09802640
Publication No. US20030036057A1

GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bansal Aruna
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapien

US-09-802-640-16

Query Match 100.0%; Score 66; DB 10; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 14

US-10-403-902A-16
Sequence 16, Application US/10403902A
Publication No. US20030224418A1

GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bansal, Aruna
APPLICANT: Kleyn, Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048B
CURRENT APPLICATION NUMBER: US/10/403,902A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 09/802,640
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapien

US-10-403-902A-16

Query Match 100.0%; Score 66; DB 15; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 15

US-10-741-600-1631

Sequence 1631, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1631
LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapiens

US-10-741-600-1631

Query Match 100.0%; Score 66; DB 17; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 16

US-10-741-600-1632
Sequence 1632, Application US/10741600
Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1632
LENGTH: 396
TYPE: PRT
ORGANISM: Homo sapiens

US-10-741-600-1632

Query Match 100.0%; Score 66; DB 17; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 79 KLVPFATELHERL 91

RESULT 17

US-10-987-454-7
Sequence 7, Application US/10987454
Publication No. US20050172359A1

GENERAL INFORMATION:
APPLICANT: Reid, Alexandra
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 9369-311
CURRENT APPLICATION NUMBER: US/10/987,454
CURRENT FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: US 60/519,606
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: US 60/579,733
PRIOR FILING DATE: 2004-06-16
NUMBER OF SEQ ID NOS: 251
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7

```
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-454-7

Query Match      100.0%; Score 66; DB 18; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 79 KLVPPFATLHERL 91

RESULT 18
US-11-017-037-33
; Sequence 33, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-037-33

Query Match      100.0%; Score 66; DB 19; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 79 KLVPPFATLHERL 91

RESULT 19
US-11-017-059-33
; Sequence 33, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-059-33

Query Match      100.0%; Score 66; DB 20; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 79 KLVPPFATLHERL 91

RESULT 20
US-09-987-107-36
; Sequence 36, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-09-987-107-36

Query Match      100.0%; Score 66; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 63 KLVPPFATLHERL 75

RESULT 21
US-10-987-454-29
; Sequence 29, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-10-987-454-29

Query Match      100.0%; Score 66; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0015;
```

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPFATLHERL 13
Db 63 KLVFPFATLHERL 75

RESULT 22

US-10-987-454-32
; Sequence 32, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio sp.
US-10-987-454-32

Query Match 100.0%; Score 66; DB 18; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPFATLHERL 13
Db 63 KLVFPFATLHERL 75

RESULT 23

US-11-017-037-36
; Sequence 36, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-11-017-037-36

Query Match 100.0%; Score 66; DB 19; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPFATLHERL 13
Db 79 KLVFPFATLHERL 91

Db 63 KLVFPFATLHERL 75

RESULT 24

US-11-017-059-36
; Sequence 36, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-11-017-059-36

Query Match 100.0%; Score 66; DB 20; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPFATLHERL 13
Db 63 KLVFPFATLHERL 75

RESULT 25

US-09-987-107-34
; Sequence 34, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-987-107-34

Query Match 100.0%; Score 66; DB 9; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFPFATLHERL 13
Db 79 KLVFPFATLHERL 91

RESULT 26
US-10-987-454-30
; Sequence 30, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: MOESTRUP, Soren
; APPLICANT: Reid, Alexandra
; APPLICANT: Meloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-987-454-30

Query Match 100.0%; Score 66; DB 18; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
Db 79 KLVPPFATELHERL 91

RESULT 27
US-11-017-037-34
; Sequence 34, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-017-037-34

Query Match 100.0%; Score 66; DB 19; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
Db 79 KLVPPFATELHERL 91

RESULT 28
US-11-017-059-34
; Sequence 34, Application US/11017059
; Publication No. US20050142639A1

; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-017-059-34

Query Match 100.0%; Score 66; DB 20; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
Db 79 KLVPPFATELHERL 91

RESULT 29
US-10-731-875A-45
; Sequence 45, Application US/10731875A
; Publication No. US20050149269A1
; GENERAL INFORMATION:
; APPLICANT: Applera Corporation
; APPLICANT: Thomas, Paul
; APPLICANT: Kejariwal, Anish
; APPLICANT: Campbell, Michael
; APPLICANT: Mi, Huaiyu
; APPLICANT: Diemer, Karen
; APPLICANT: Guo, Nan
; APPLICANT: Ladunga, Istvan
; APPLICANT: Lazareva, Betty
; APPLICANT: Muruganujan, Anushya
; APPLICANT: Rabkin, Steven
; APPLICANT: Vandergriff, Jody
; APPLICANT: Doremieux, Olivier
; TITLE OF INVENTION: Browsable Database For Biological Use
; FILE REFERENCE: 9692-000029
; CURRENT APPLICATION NUMBER: US/10/731,875A
; CURRENT FILING DATE: 2003-12-09
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Exemplary Protein Sequence.
US-10-731-875A-45

Query Match 68.2%; Score 45; DB 18; Length 85;
Best Local Similarity 69.2%; Pred. No. 1.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
Db 28 KLVPPFATELQAQL 40

RESULT 30
US-10-316-253-279
; Sequence 279, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 279
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-279

Query Match 62.1%; Score 41; DB 14; Length 258;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHE 11
||| |||||
Db 140 KLEPLATLHK 150

RESULT 31
US-10-316-253-281
; Sequence 281, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-281

Query Match 62.1%; Score 41; DB 14; Length 258;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHE 11
||| |||||
Db 140 KLEPLATLHK 150

RESULT 32
US-10-316-253-283
; Sequence 283, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin

; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 283
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-283

Query Match 62.1%; Score 41; DB 14; Length 258;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHE 11
||| |||||
Db 140 KLEPLATLHK 150

RESULT 33
US-10-417-700A-79
; Sequence 79, Application US/10417700A
; Publication No. US20040033581A1
; GENERAL INFORMATION:
; APPLICANT: ECOPIA BIOSCIENCES INC.
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STAFRA, Alfredo
; APPLICANT: FARNET, Chris
; TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribos
; FILE REFERENCE: 3002-14US
; CURRENT APPLICATION NUMBER: US/10/417,700A
; CURRENT FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Streptomyces aizewensis strain NRRL B-11277
US-10-417-700A-79

Query Match 62.1%; Score 41; DB 15; Length 472;
Best Local Similarity 72.7%; Pred. No. 72;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VPPFATLHERL 13
||| |||||
Db 218 VPPFATLHERL 228

RESULT 34
US-10-767-701-61044
; Sequence 61044, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 61044
; LENGTH: 166

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; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; LOCATION: (1)..(237)
; OTHER INFORMATION: Clone ID: 9300886.pap
US-10-767-701-61044

Query Match      60.6%; Score 40; DB 16; Length 166;
Best Local Similarity 72.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPFATLHERL 13
   :|||||:|
Db 1 MPFATLTKRL 11

RESULT 35
US-10-425-115-242838
; Sequence 242838, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242838
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(237)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: MRT4577_15304C.1.pap
US-10-425-115-242838

Query Match      60.6%; Score 40; DB 16; Length 237;
Best Local Similarity 88.9%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LVPFATELH 10
   :|||||:|
Db 119 LVPFATEEH 127

RESULT 36
US-10-437-963-120340
; Sequence 120340, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120340
; LENGTH: 239
; TYPE: PRT
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; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(239)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2346C.1.pap
US-10-437-963-120340

Query Match      60.6%; Score 40; DB 16; Length 239;
Best Local Similarity 72.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPFATLHERL 13
   :|||||:|
Db 1 MPFATLTKRL 11

RESULT 37
US-09-987-107-20
; Sequence 20, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-987-107-20

Query Match      60.6%; Score 40; DB 9; Length 266;
Best Local Similarity 53.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPFATLHERL 13
   |||:|:|:|
Db 185 KLAPYSNELQQRL 197

RESULT 38
US-10-987-454-17
; Sequence 17, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 17
; LENGTH: 266
; TYPE: PRT
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; ORGANISM: Oryctolagus cuniculus
US-10-987-454-17

Query Match 60.6%; Score 40; DB 18; Length 266;
Best Local Similarity 53.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13
|||::|||:
Db 185 KLAPYSNELQRL 197

RESULT 39

US-11-017-037-20
; Sequence 20, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-11-017-037-20

Query Match 60.6%; Score 40; DB 19; Length 266;
Best Local Similarity 53.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13
|||::|||:
Db 185 KLAPYSNELQRL 197

RESULT 40

US-11-017-059-20
; Sequence 20, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus

US-11-017-059-20

Query Match 60.6%; Score 40; DB 20; Length 266;
Best Local Similarity 53.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13
|||::|||:
Db 185 KLAPYSNELQRL 197

RESULT 41

US-10-437-963-195972
; Sequence 195972, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 195972
; LENGTH: 1809
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91869C.1.pep
US-10-437-963-195972

Query Match 60.6%; Score 40; DB 16; Length 1809;
Best Local Similarity 53.8%; Pred. No. 5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13
|||::|||:
Db 464 KLISFVDEAHERI 476

RESULT 42

US-10-437-963-177544
; Sequence 177544, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 177544
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_75185C.1.pep
US-10-437-963-177544

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Query Match      59.1%; Score 39; DB 16; Length 86;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVPPFATELHER 12
   :|:|:|:|:|
Db 73 EIVRFSTDIHER 84

RESULT 43
US-10-437-963-152800
; Sequence 152800, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152800
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(117)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52815C.1.pep
US-10-437-963-152800

Query Match      59.1%; Score 39; DB 16; Length 117;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATELHER 12
   :|:|:|:|:|
Db 63 ELVFFTGLLHER 74

RESULT 44
US-10-425-115-336871
; Sequence 336871, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336871
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(143)
; OTHER INFORMATION: unsure at all Xaa locations

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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70397C.1.pep
US-10-425-115-336871

Query Match      59.1%; Score 39; DB 16; Length 143;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVPFATELHER 12
   :|:|:|:|:|
Db 133 IVRFCTEVHER 143

RESULT 45
US-09-815-242-10585
; Sequence 10585, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haseibeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10585
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10585

Query Match      59.1%; Score 39; DB 9; Length 220;
Best Local Similarity 87.5%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PFATELHE 11
   :|:|:|:|
Db 22 PFITELHE 29

Search completed: September 1, 2005, 16:45:05
Job time : 164 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 16:12:34 ; Search time 166 Seconds
(without alignments)
30.288 Million cell updates/sec

Title: US-09-993-366-1

Perfect score: 66

Sequence: 1 KLVPFATLHERL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04.*

1: geneseqp1980s.*

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3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	13	6 ABR62228	Abp62228 Apolipop
2	66	100.0	13	8 ADE52384	Ade52384 Human apo
3	66	100.0	85	8 ADP87442	Adp87442 Human apo
4	66	100.0	85	8 ADP87439	Adp87439 Pig apoli
5	66	100.0	85	8 ADP87440	Adp87440 Baboon ap
6	66	100.0	85	8 ADP87441	Adp87441 Monkey ap
7	66	100.0	183	2 AAR39482	Aar39482 Human apo
8	66	100.0	333	2 AAR39495	Aar39495 Human apo
9	66	100.0	333	2 AAR39488	Aar39488 Human apo
10	66	100.0	333	2 AAR39481	Aar39481 Human apo
11	66	100.0	333	2 AAR39497	Aar39497 Human apo
12	66	100.0	333	2 AAR39490	Aar39490 Human apo
13	66	100.0	337	2 AAR39492	Aar39492 Human apo
14	66	100.0	337	2 AAR39494	Aar39494 Human apo
15	66	100.0	342	2 AAR39487	Aar39487 Human apo
16	66	100.0	342	2 AAR39491	Aar39491 Human apo
17	66	100.0	342	2 AAR39489	Aar39489 Human apo
18	66	100.0	342	2 AAR39498	Aar39498 Human apo
19	66	100.0	342	2 AAR39496	Aar39496 Human apo
20	66	100.0	346	2 AAR39493	Aar39493 Human apo
21	66	100.0	363	2 AAR39478	Aar39478 Human apo
22	66	100.0	363	2 AAR39479	Aar39479 Human apo
23	66	100.0	373	2 AAR39486	Aar39486 Human apo
24	66	100.0	377	2 AAR39502	Aar39502 Human apo
25	66	100.0	377	2 AAR39443	Aar39443 Human apo

26	66	100.0	377	2 AAR45244	Aar45244 Human apo
27	66	100.0	377	2 AAR39501	Aar39501 Human apo
28	66	100.0	377	2 AAR45242	Aar45242 Human apo
29	66	100.0	377	2 AAR39480	Aar39480 Human apo
30	66	100.0	377	2 AAR39499	Aar39499 Human apo
31	66	100.0	377	2 AAR39500	Aar39500 Human apo
32	66	100.0	377	2 AAR45243	Aar45243 Human apo
33	66	100.0	382	4 AAB90663	Aab90663 Human sec
34	66	100.0	396	4 AAB90664	Aab90664 Human sec
35	66	100.0	396	5 AAO15885	Aao15885 Human apo
36	66	100.0	396	5 AAU10862	Aau10862 Human apo
37	66	100.0	396	5 AAU10863	Aau10863 Human apo
38	66	100.0	396	5 AAU10865	Aau10865 Human apo
39	66	100.0	396	5 AAU10867	Aau10867 Human apo
40	66	100.0	396	5 AAU10866	Aau10866 Human apo
41	66	100.0	396	5 AAU10869	Aau10869 Human apo
42	66	100.0	396	5 AAU10861	Aau10861 Human apo
43	66	100.0	396	5 AAU10868	Aau10868 Human apo
44	66	100.0	396	5 AAU10860	Aau10860 Human apo
45	66	100.0	396	5 AAU10864	Aau10864 Human apo
46	66	100.0	396	7 ADE60278	Ade60278 Human Pro
47	66	100.0	396	8 ADQ39968	Adq39968 Human myo
48	66	100.0	396	8 ADQ39969	Adq39969 Human myo
49	53	80.3	328	2 AAR39484	Aar39484 Human apo
50	53	80.3	337	2 AAR39485	Aar39485 Human apo
51	45	68.2	85	8 ADP87438	Adp87438 Chicken a
52	45	68.2	438	6 ABM69115	Abm69115 Photorhab
53	42	63.6	434	4 ABB66417	Abb66417 Drosophil
54	41	62.1	258	7 ADF30720	Adf30720 Rat angio
55	41	62.1	258	7 ADF30718	Adf30718 Rat angio
56	41	62.1	258	7 ADF30716	Adf30716 Rat angio
57	41	62.1	472	7 ADG33820	Adg33820 Actinomyc
58	40	60.6	49	6 ABR44041	Abra44041 Rabbit Ap
59	40	60.6	242	4 ABG28667	Abg28667 Novel hum
60	39	59.1	242	4 ABM69659	Abm69659 Photorhab
61	39	59.1	220	6 AAU34992	Aau34992 Enterococ
62	39	59.1	220	6 ABU29095	Abu29095 Protein e
63	39	59.1	397	8 ADN21067	Adn21067 Bacterial
64	39	59.1	397	8 ADN21068	Adn21068 Bacterial
65	39	59.1	815	4 ABG19101	Abg19101 Novel hum
66	39	59.1	2796	6 ABU79133	Abu79133 Mycobacte
67	39	59.1	2796	7 ADF43394	Adf43394 Mycobacte
68	39	59.1	2796	8 ADQ26440	Adq26440 Mycobacte
69	39	59.1	2796	8 ADR88334	Adr88334 Mycobacte
70	39	59.1	3069	8 ADQ26432	Adq26432 Mycobacte
71	39	59.1	3069	8 ADR88327	Adr88327 Mycobacte
72	39	59.1	3070	4 AAG81195	Aag81195 Mycobacte
73	39	59.1	3076	8 ADQ26433	Adq26433 Mycobacte
74	39	59.1	3076	8 ADR88328	Adr88328 Mycobacte
75	38	57.6	15	2 AAY42559	Aay42559 Apolipop
76	38	57.6	213	4 ABG03485	Abg03485 Novel hum
77	38	57.6	243	7 ADF04137	Adf04137 Bacterial
78	38	57.6	261	5 AAU99616	Aau99616 Agrobacte
79	38	57.6	262	7 ADJ83088	Adj83088 Apolipop
80	38	57.6	314	7 ADC23743	Adc23743 Protein s
81	38	57.6	314	8 ADH35844	Adh35844 Chemical
82	38	57.6	314	8 ADG93545	Adg93545 Nitrilase
83	38	57.6	314	8 ADI62142	Adi62142 Nitrilase
84	38	57.6	319	7 ADI64263	Adi64263 Nitrilase
85	38	57.6	319	7 ADM25798	Adm25798 Hyperther
86	38	57.6	391	7 ADE60276	Ade60276 Rat Prote
87	38	57.6	391	7 ADF30675	Adf30675 Rat angio
88	38	57.6	391	7 ADF30677	Adf30677 Rat angio
89	38	57.6	391	7 ADF30679	Adf30679 Rat angio
90	38	57.6	405	8 ADS25206	Ads25206 Bacterial
91	38	57.6	405	8 ADS44961	Ads44961 Bacterial
92	38	57.6	405	8 ADS25821	Ads25821 Bacterial
93	38	57.6	405	8 ADS26010	Ads26010 Bacterial
94	38	57.6	405	8 ADS22551	Ads22551 Bacterial
95	38	57.6	428	6 ABU17846	Abu17846 Protein e
96	38	57.6	428	8 ADS28450	Ads28450 Bacterial
97	38	57.6	429	6 ABU17531	Abu17531 Protein e
98	38	57.6	473	8 ADJ49354	Adj49354 Oil-assoc

99 38 57.6 492 7 ABO67691
100 38 57.6 571 7 ADC51490 Bacterial

ALIGNMENTS

RESULT 1
ABR62228
ID ABR62228 standard; peptide; 13 AA.
XX AC AC
XX ABR62228;
XX 08-SEP-2003 (first entry)
XX Apolipoprotein marker predictive of insulin resistance.
XX DE Apolipoprotein; human; insulin resistance; marker.
XX KW Homo sapiens.
XX OS
XX PN WO2003046000-A2.
XX PD
XX 05-JUN-2003.
XX 31-OCT-2002; 2002WO-CA001660.
XX PF
XX 21-NOV-2001; 2001US-00993366.
XX PR
XX (SYNX-) SYN.X PHARMA INC.
XX PA
XX Jackowski G, Marshall J;
XX PI
XX WPI; 2003-493400/46.
XX DR
XX New biopolymer marker, useful for indicating, for determining risk-
PT assessment or for identifying therapeutic avenues related to, a disease
- PT state e.g., Alzheimer's disease.
XX
XX Claim 1; Page 43; 43pp; English.
XX PS
XX The present invention relates to the use of mass spectrometry to
CC elucidate particular biopolymer markers indicative or predictive of a
CC particular disease state, and especially biopolymer markers whose up-
CC regulation, down-regulation or relative presence in disease versus normal
CC states has been determined to be useful in disease state assessment and
CC therapeutic target recognition, development and validation. As a result
CC of these procedures, the present apolipoprotein A-IV precursor protein
CC was identified as a marker predictive of insulin resistance. The presence
CC or absence of such markers can be used in disease risk assessment and in
CC the development of therapeutic avenues against the disease
XX SQ Sequence 13 AA;

Query Match 100.0%; Score 66; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVPFFATELHERL 13
Db 1 KLVPFFATELHERL 13
RESULT 2
ADE52384
ID ADE52384 standard; peptide; 13 AA.
XX AC ADE52384;
XX 29-JAN-2004 (first entry)
XX DE Human apolipoprotein biopolymer marker #2.
XX

Query Match 100.0%; Score 66; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVPFFATELHERL 13
Db 1 KLVPFFATELHERL 13
RESULT 3
ADP87442
ID ADP87442 standard; protein; 85 AA.
XX AC ADP87442;
XX 09-SEP-2004 (first entry)
XX DE Human apolipoprotein A (APO-A) precursor protein.
XX KW Browseable database system; ontology; protein analysis;
XX gene product classification; genomic analysis; apolipoprotein A; APO-A;
XX human.
XX OS Homo sapiens.
XX PN WO2004053769-A2.
XX PD 24-JUN-2004.
XX 09-DEC-2003; 2003WO-US038935.
XX PF 09-DEC-2002; 2002US-0431879P.
XX PR
XX (APPL-) APPLERA CORP.
XX PA

KW human; apolipoprotein biopolymer marker; disease state regulation;
KW therapeutic avenue.
XX OS Homo sapiens.
XX PN US2003100014-A1.
XX 29-MAY-2003.
XX 23-NOV-2001; 2001US-00991809.
XX PF
XX 23-NOV-2001; 2001US-00991809.
XX PR
XX (JACK/) JACKOMSKI G.
XX (MARS/) MARSHALL J.
XX Jackowski G, Marshall J;
XX WPI; 2004-031198/03.
XX DR
XX New apolipoprotein biopolymer marker useful for indicating at least one
PT particular disease state, such as, Type II diabetes, using e.g. mass
PT spectrometric analysis.
XX PS
XX Claim 1; Page 11; 17pp; English.
XX The invention relates to an apolipoprotein biopolymer marker or its
CC analyte useful in indicating a particular disease state. The
CC apolipoprotein biopolymer marker is useful for regulating a disease state
CC by controlling the presence or absence of apolipoprotein biopolymer
CC marker. The apolipoprotein biopolymer marker or a diagnostic kit is
CC useful for identifying therapeutic avenues related to a disease state,
CC which involves conducting an analysis by using the diagnostic kit and
CC interacting with apolipoprotein biopolymer marker. The present sequence
CC represents the amino acid sequence of a human apolipoprotein biopolymer
CC marker.
XX SQ Sequence 13 AA;

Query Match 100.0%; Score 66; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLVPFFATELHERL 13
Db 1 KLVPFFATELHERL 13
RESULT 3
ADP87442
ID ADP87442 standard; protein; 85 AA.
XX AC ADP87442;
XX 09-SEP-2004 (first entry)
XX DE Human apolipoprotein A (APO-A) precursor protein.
XX KW Browseable database system; ontology; protein analysis;
XX gene product classification; genomic analysis; apolipoprotein A; APO-A;
XX human.
XX OS Homo sapiens.
XX PN WO2004053769-A2.
XX PD 24-JUN-2004.
XX 09-DEC-2003; 2003WO-US038935.
XX PF 09-DEC-2002; 2002US-0431879P.
XX PR
XX (APPL-) APPLERA CORP.
XX PA

PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX WPI; 1993-258676/32.
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX PT and/or treatment of hypercholesterolaemia.
XX
XX Claim 7; Page 31-32 and Page 4; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apoAIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such mutants are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR39481 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 333 AA;

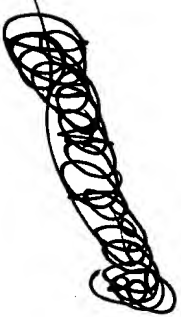
Query Match 100.0%; Score 66; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 60 KLVPPFATELHERL 72
|||||


RESULT 10
AAR39481
ID AAR39481 standard; protein; 333 AA.
XX
XX AC AAR39481;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX
XX Human apoAIV mutein P(deltaC44).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecithin-cholesterol-acyltransferase; LCAT.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Protein 2..333
XX /label= P(deltaC44)
XX /note= "the 44 C-terminal amino acids of human apoAIV
XX have been deleted"
XX
XX WO9315198-A1.
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92PR-00000806.
XX
XX (RHON) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX PT and/or treatment of hypercholesterolaemia.
XX

PS Claim 7; Page 31-32 and Page 4; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apoAIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such mutants are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR39481 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 333 AA;

Query Match 100.0%; Score 66; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 60 KLVPPFATELHERL 72
|||||


RESULT 11
AAR39497
ID AAR39497 standard; protein; 333 AA.
XX
XX AC AAR39497;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX
XX Human apoAIV mutein P(delta h5-6).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecithin-cholesterol-acyltransferase; LCAT.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 14..40
XX /note= "helix 1"
XX Region 41..62
XX /note= "helix 2"
XX Region 63..95
XX /note= "helix 3"
XX Region 96..117
XX /note= "helix 4"
XX Misc-difference 117..118
XX /note= "helices 5-6 have been deleted from between these
XX two sites"
XX
XX Region 118..139
XX /note= "helix 7"
XX Region 140..161
XX /note= "helix 8"
XX Region 162..183
XX /note= "helix 9"
XX Region 184..205
XX /note= "helix 10"
XX Region 206..223
XX /note= "helix 11"
XX Region 224..245
XX /note= "helix 12"
XX Region 246..267
XX /note= "helix 13"
XX Region 268..289
XX /note= "helix 14"
XX Region 290..333
XX /note= "helix 15"
XX

XX WO9315198-A1.
 XX PD
 XX 05-AUG-1993.
 XX PF 26-JAN-1993; 93WO-FR0000073.
 XX PR 27-JAN-1992; 92FR-00000806.
 XX PA (RHON) RHONE POULENC RORER SA.
 XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39497 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 333 AA;
 PS Query Match 100.0%; Score 66; DB 2; Length 333;
 Best Local Similarity 100.0%; Pred. NO. 0.00078;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVPFATLHERL 13
 Db 60 KLVPFATLHERL 72
 RESULT 12
 ID AAR39490 standard; protein; 333 AA.
 AC AAR39490;
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 DE Human apoAIV mutein P(delta h9-10).
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Region 14..40
 FT /note= "helix 1"
 FT Region 41..62
 FT /note= "helix 2"
 FT Region 63..95
 FT /note= "helix 3"
 FT Region 96..117
 FT /note= "helix 4"
 FT Region 118..139
 FT /note= "helix 5"
 FT Region 140..161

FT Region /note= "helix 6"
 FT 162..183
 FT /note= "helix 7"
 FT Region 184..205
 FT /note= "helix 8"
 FT Misc-difference 205..206
 FT /note= "helices 9-10 have been deleted from between these
 FT two sites"
 FT Region 206..223
 FT /note= "helix 11"
 FT Region 224..245
 FT /note= "helix 12"
 FT Region 246..267
 FT /note= "helix 13"
 FT Region 268..289
 FT /note= "helix 14"
 FT Region 290..333
 FT /note= "helix 15"
 XX WO9315198-A1.
 XX PD 05-AUG-1993.
 XX PF 26-JAN-1993; 93WO-FR0000073.
 XX PR 27-JAN-1992; 92FR-00000806.
 XX PA (RHON) RHONE POULENC RORER SA.
 XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39490 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 333 AA;
 PS Query Match 100.0%; Score 66; DB 2; Length 333;
 Best Local Similarity 100.0%; Pred. NO. 0.00078;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVPFATLHERL 13
 Db 60 KLVPFATLHERL 72
 RESULT 13
 ID AAR39492 standard; protein; 337 AA.
 AC AAR39492;
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 DE Human apoAIV mutein P(delta h11-12).
 XX

DR WPI; 1993-258676/32.
 XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 PS
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39494 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 337 AA;
 Query Match 100.0%; Score 66; DB 2; Length 337;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPPFATELHERL 13
 DB 60 KLVPPFATELHERL 72
 RESULT 15
 AAR39487
 ID AAR39487 standard; protein; 342 AA.
 XX
 XX AAR39487;
 XX
 DT 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apoAIV mutein P(tag-deltaC44).
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
 XX
 OS Synthetic.
 Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= tag decapeptide
 FT /note= "allows rapid, single stage purification without
 FT affecting the properties of the mature mutein"
 FT Protein 11..342
 FT /label= P(deltaC44)
 FT /note= "the 44 C-terminal amino acids of mature human
 FT apoAIV have been deleted"
 XX
 PN WO9315198-A1.
 XX
 XX 05-AUG-1993.
 XX
 XX 26-JAN-1993; 93WO-FR000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Deneffe P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT

PT and/or treatment of hypercholesterolaemia.
 XX
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39487 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 342 AA;
 Query Match 100.0%; Score 66; DB 2; Length 342;
 Best Local Similarity 100.0%; Pred. No. 0.0008;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPPFATELHERL 13
 DB 69 KLVPPFATELHERL 81
 RESULT 16
 AAR39491
 ID AAR39491 standard; protein; 342 AA.
 XX
 XX AAR39491;
 XX
 DT 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apoAIV mutein P(tag-delta h9-10).
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
 XX
 OS Synthetic.
 Key Location/Qualifiers
 FH Peptide 1..10
 FT /label= tag decapeptide
 FT /note= "allows rapid, single stage purification without
 FT affecting the properties of the mature mutein"
 FT Region 23..49
 FT /note= "helix 1"
 FT Region 50..71
 FT /note= "helix 2"
 FT Region 72..104
 FT /note= "helix 3"
 FT Region 105..126
 FT /note= "helix 4"
 FT Region 127..148
 FT /note= "helix 5"
 FT Region 149..170
 FT /note= "helix 6"
 FT Region 171..192
 FT /note= "helix 7"
 FT Region 193..214
 FT /note= "helix 8"
 FT Misc-difference 214..215
 FT /note= "helices 9-10 have been deleted from between these
 FT two sites"
 FT Region 215..232
 FT /note= "helix 11"
 FT Region 233..254
 FT /note= "helix 12"
 FT

FT Region 255..276
 FT /note= "helix 13"
 FT 277..298
 FT /note= "helix 14"
 FT Region 299..342
 FT /note= "helix 15"
 FT FT
 XX
 XX WO9315198-A1.
 XX
 XX
 XX 05-AUG-1993.
 XX
 XX 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apo-lipoprotein AIV mutant polypeptide(s) - useful for drug design
 FT and/or treatment of hypercholesterolaemia.
 FT
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39489 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 342 AA;
 XX
 XX Query Match 100.0%; Score 66; DB 2; Length 342;
 XX Best Local Similarity 100.0%; Pred. No. 0.0008;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 KLVPFATELHERL 13
 Db |||||
 69 KLVPFATELHERL 81
 RESULT 17
 ID AAR39489 standard; protein; 342 AA.
 XX
 XX AAR39489;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 XX Human apoAIV mutein P(tag-delta h7-8).
 XX
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT 1..10
 FT /label= tag decapeptide
 FT /note= "allows rapid, single stage purification without
 FT affecting the properties of the mature mutein"
 FT 23..49
 FT Region

FT Region /note= "helix 1"
 FT 50..71
 FT /note= "helix 2"
 FT Region 72..104
 FT /note= "helix 3"
 FT Region 105..126
 FT /note= "helix 4"
 FT Region 127..148
 FT /note= "helix 5"
 FT Region 149..170
 FT /note= "helix 6"
 FT Misc-difference 170..171
 FT /note= "helices 7-8 have been deleted from between these
 FT two sites"
 FT 171..192
 FT /note= "helix 9"
 FT Region 193..214
 FT /note= "helix 10"
 FT Region 215..232
 FT /note= "helix 11"
 FT Region 233..254
 FT /note= "helix 12"
 FT Region 255..276
 FT /note= "helix 13"
 FT Region 277..298
 FT /note= "helix 14"
 FT Region 299..342
 FT /note= "helix 15"
 FT
 FT WO9315198-A1.
 XX
 XX 05-AUG-1993.
 XX
 XX 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apo-lipoprotein AIV mutant polypeptide(s) - useful for drug design
 FT and/or treatment of hypercholesterolaemia.
 FT
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39489 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 342 AA;
 XX
 XX Query Match 100.0%; Score 66; DB 2; Length 342;
 XX Best Local Similarity 100.0%; Pred. No. 0.0008;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 KLVPFATELHERL 13
 Db |||||
 69 KLVPFATELHERL 81
 RESULT 18
 ID AAR39489 standard; protein; 342 AA.
 XX
 XX AAR39489;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 XX Human apoAIV mutein P(tag-delta h7-8).
 XX
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT 1..10
 FT /label= tag decapeptide
 FT /note= "allows rapid, single stage purification without
 FT affecting the properties of the mature mutein"
 FT 23..49
 FT Region

QY 1 KLVPFATELHERL 13
 Db |||||
 69 KLVPFATELHERL 81

RESULT 18

AAR39498
ID AAR39498 standard; protein; 342 AA.
AC AAR39498;
XX
XX 25-MAR-2003 (revised)
DT 28-JAN-1994 (first entry)
XX Human apoAIV mutain P(tag-delta h5-6).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= tag decapeptide
FT /note= "allows rapid, single stage purification without
FT affecting the properties of the mature mutain"
FT Region 23..49
FT /note= "helix 1"
FT Region 50..71
FT /note= "helix 2"
FT Region 72..104
FT /note= "helix 3"
FT Region 105..126
FT /note= "helix 4"
FT Misc-difference 126..127
FT /note= "helices 5-6 have been deleted from between these
FT two sites"
FT Region 127..148
FT /note= "helix 7"
FT Region 149..170
FT /note= "helix 8"
FT Region 171..192
FT /note= "helix 9"
FT Region 193..214
FT /note= "helix 10"
FT Region 215..232
FT /note= "helix 11"
FT Region 233..254
FT /note= "helix 12"
FT Region 255..276
FT /note= "helix 13"
FT Region 277..298
FT /note= "helix 14"
FT Region 299..342
FT /note= "helix 15"
XX WO9315198-A1.
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92FR-0000806.
XX (RHON) RHONE POULENC RORER SA.
XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
PT and/or treatment of hypercholesterolaemia.
PT
XX Claim 7; Page 31-32 and Page 5; 42pp; French.
PS
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
CC but is mainly found in the plasma in unassociated form. The apoAIV
CC mediates inverse transport of cholesterol. The invention covers

CC polypeptides which are derived from apoAIV by deletion of at least 10
CC terminal amino acids, by deletion of a helix or pair of helices, by
CC addition of a heterologous polypeptide portion or by a point mutation.
CC Such mutains are useful in the design of hypocholesterolaemic drugs to
CC treat hypercholesterolaemia and atherosclerosis. AAR39498 is a
CC specifically claimed mutain and the sequence has been compiled from the
CC wild-type sequence (see AAR39443) and the description given in the
CC disclosure; the mutant sequence is not shown in the specification.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 342 AA;
Query Match 100.0%; Score 66; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFATELHERL 13
DB 69 KLVFFATELHERL 81
RESULT 19
AAR39496
ID AAR39496 standard; protein; 342 AA.
XX
AC AAR39496;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1994 (first entry)
XX
DE Human apoAIV mutain P(tag-delta h13-14).
KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= tag decapeptide
FT /note= "allows rapid, single stage purification without
FT affecting the properties of the mature mutain"
FT Region 23..49
FT /note= "helix 1"
FT Region 50..71
FT /note= "helix 2"
FT Region 72..104
FT /note= "helix 3"
FT Region 105..126
FT /note= "helix 4"
FT Region 127..148
FT /note= "helix 5"
FT Region 149..170
FT /note= "helix 6"
FT Region 171..192
FT /note= "helix 7"
FT Region 193..214
FT /note= "helix 8"
FT Region 215..236
FT /note= "helix 9"
FT Region 237..258
FT /note= "helix 10"
FT Region 259..276
FT /note= "helix 11"
FT Region 277..298
FT /note= "helix 12"
FT Misc-difference 298..299
FT /note= "helices 13-14 have been deleted from between
FT these two sites"
FT Region 299..342
FT /note= "helix 15"
XX

PN WO9315198-A1.
 XX
 PD
 XX
 XX 05-AUG-1993.
 PF 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 XX
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 PS Human apolipoprotein AIV is a major component of chylomicrons in lymph
 XX but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39496 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 342 AA;
 SQ
 Query Match 100.0%; Score 66; DB 2; Length 342;
 Best Local Similarity 100.0%; Pred. No. 0.0008;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPPFATLHERL 13
 DB 69 KLVPPFATLHERL 81
 RESULT 20
 AAR39493
 ID AAR39493 standard; protein; 346 AA.
 AC
 AC AAR39493;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 XX Human apoAIV mutein P(tag-delta h11-12).
 DE
 XX
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH 1. .10
 FT Peptide /label= tag_decapeptide
 FT /note= "allows rapid, single stage purification without
 FT affecting the properties of the mature mutein"
 FT 23. .49
 FT Region /note= "helix 1"
 FT 50. .71
 FT Region /note= "helix 2"
 FT 72. .104
 FT Region /note= "helix 3"
 FT 105. .126
 FT Region /note= "helix 4"
 FT

FT Region 127. .148
 FT /note= "helix 5"
 FT 149. .170
 FT /note= "helix 6"
 FT 171. .192
 FT /note= "helix 7"
 FT 193. .214
 FT /note= "helix 8"
 FT 215. .236
 FT /note= "helix 9"
 FT 237. .258
 FT /note= "helix 10"
 FT Misc-difference 258. .259
 FT /note= "helices 11-12 have been deleted from between
 FT these two sites"
 FT 259. .280
 FT /note= "helix 13"
 FT 281. .302
 FT /note= "helix 14"
 FT 303. .346
 FT /note= "helix 15"
 XX
 XX WO9315198-A1.
 XX
 XX 05-AUG-1993.
 PD
 PD 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 PR
 PR (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 XX
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 PS Human apolipoprotein AIV is a major component of chylomicrons in lymph
 XX but is mainly found in the plasma in unassociated form. The apoAIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39493 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 346 AA;
 SQ
 Query Match 100.0%; Score 66; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 0.00081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPPFATLHERL 13
 DB 69 KLVPPFATLHERL 81
 RESULT 21
 AAR39478
 ID AAR39478 standard; protein; 363 AA.
 XX
 XX AAR39478;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 DT

XX DE Human apoAIV mutain P(deltaN13, R93G).

XX KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

KW KW coronary disease; chylomicron; cholesterol transport; plaque deposition;

KW KW lecithin-cholesterol-acyltransferase; LCAT.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Protein 1. .363

FT /label= (deltaN13, R93G)

FT /note= "the 13 N-terminal amino acids of human apoAIV

FT have been deleted and wild-type Arg93 has been substd. by

FT Gly"

FT Misc-difference 79

FT /note= "R93G"

XX PN WO9315198-A1.

XX PD 05-AUG-1993.

XX PF 26-JAN-1993; 93WO-FR0000073.

XX PR 27-JAN-1992; 92FR-00000806.

XX PA (RHON) RHONE POULENC RORER SA.

XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;

XX WPI; 1993-258676/32.

XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design

XX and/or treatment of hypercholesterolaemia.

XX Claim 7; Page 31-32 and Page 4; 42pp; French.

XX Human apolipoprotein AIV is a major component of chylomicrons in lymph

CC but is mainly found in the plasma in unassociated form. The apoAIV

CC mediates inverse transport of cholesterol. The invention covers

CC polypeptides which are derived from apoAIV by deletion of at least 10

CC terminal amino acids, by deletion of a helix or pair of helices, by

CC addition of a heterologous polypeptide portion or by a point mutation.

CC Such mutants are useful in the design of hypocholesterolaemic drugs to

CC treat hypercholesterolaemia and atherosclerosis. AAR39478 is a

CC specifically claimed mutain and the sequence has been compiled from the

CC wild-type sequence (see AAR39443) and the description given in the

CC disclosure; the mutant sequence is not shown in the specification.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 363 AA;

Query Match 100.0%; Score 66; DB 2; Length 363;

Best Local Similarity 100.0%; Pred. No. 0.00085;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13

Db 46 KLVPFATLHERL 58

RESULT 22

ID AAR39479 standard; protein; 363 AA.

AC AAR39479;

XX 25-MAR-2003 (revised)

DT 28-JAN-1994 (first entry)

XX Human apoAIV mutain P(deltaN13).

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

XX KW coronary disease; chylomicron; cholesterol transport; plaque deposition;

XX KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1. .10

KW KW coronary disease; chylomicron; cholesterol transport; plaque deposition;

XX KW lecithin-cholesterol-acyltransferase; LCAT.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Protein 1. .363

FT /label= P(deltaN13)

FT /note= "the 13 N-terminal amino acids of mature human

FT apoAIV have been deleted"

XX PN WO9315198-A1.

XX PD 05-AUG-1993.

XX PF 26-JAN-1993; 93WO-FR0000073.

XX PR 27-JAN-1992; 92FR-00000806.

XX PA (RHON) RHONE POULENC RORER SA.

XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;

XX WPI; 1993-258676/32.

XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design

XX and/or treatment of hypercholesterolaemia.

XX Claim 7; Page 31-32 and Page 4; 42pp; French.

XX Human apolipoprotein AIV is a major component of chylomicrons in lymph

CC but is mainly found in the plasma in unassociated form. The apoAIV

CC mediates inverse transport of cholesterol. The invention covers

CC polypeptides which are derived from apoAIV by deletion of at least 10

CC terminal amino acids, by deletion of a helix or pair of helices, by

CC addition of a heterologous polypeptide portion or by a point mutation.

CC Such mutants are useful in the design of hypocholesterolaemic drugs to

CC treat hypercholesterolaemia and atherosclerosis. AAR39479 is a

CC specifically claimed mutain and the sequence has been compiled from the

CC wild-type sequence (see AAR39443) and the description given in the

CC disclosure; the mutant sequence is not shown in the specification.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 363 AA;

Query Match 100.0%; Score 66; DB 2; Length 363;

Best Local Similarity 100.0%; Pred. No. 0.00085;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATLHERL 13

Db 46 KLVPFATLHERL 58

RESULT 23

ID AAR39486 standard; protein; 373 AA.

AC AAR39486;

XX 25-MAR-2003 (revised)

DT 28-JAN-1994 (first entry)

XX Human apoAIV mutain P(tag-deltaN13).

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

XX KW coronary disease; chylomicron; cholesterol transport; plaque deposition;

XX KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1. .10

```

FT FT /label= tag,decapeptide
FT FT /note= "allows rapid, single stage purification without
FT FT affecting the properties of the mature mutein"
FT Protein
FT 11..373
FT /label= P(deltaN13)
FT /note= "the 13 N-terminal amino acids of mature human
FT FT apoAIV have been deleted"
XX PN WO9315198-A1.
XX XX
XX PD 05-AUG-1993.
XX XX
XX PF 26-JAN-1993; 93WO-FR000073.
XX XX
XX PR 27-JAN-1992; 92FR-00000806.
XX XX
XX PA (RHON ) RHONE POULENC RORER SA.
XX XX
XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX DR WPI; 1993-258676/32.
XX XX
XX PF New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
FT FT and/or treatment of hypercholesterolaemia.
XX PS Claim 7; Page 31-32 and Page 4; 42pp; French.
XX CC Human apolipoprotein AIV is a major component of chylomicrons in lymph
CC but is mainly found in the plasma in unassociated form. The apoAIV
CC mediates inverse transport of cholesterol. The invention covers
CC polypeptides which are derived from apoAIV by deletion of at least 10
CC terminal amino acids, by deletion of a helix or pair of helices, by
CC addition of a heterologous polypeptide portion or by a point mutation.
CC Such muteins are useful in the design of hypocholesterolaemic drugs to
CC treat hypercholesterolaemia and atherosclerosis. AAR39486 is a
CC specifically claimed mutein and the sequence has been compiled from the
CC wild-type sequence (see AAR39443) and the description given in the
CC disclosure; the mutant sequence is not shown in the specification.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 373 AA;

Query Match 100.0%; Score 66; DB 2; Length 373;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 56 KLVPFATELHERL 68
|||||
|||||

RESULT 24
AAR39502
ID AAR39502 standard; protein; 377 AA.
XX AC AAR39502;
XX DT 25-MAR-2003 (revised)
XX DT 28-JAN-1994 (first entry)
XX DE Human apoAIV mutein P(D5K).
XX KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecitithin-cholesterol-acyltransferase; LCAT.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Protein 2..377
XX FT /note= "mature P(D5K)"
XX FT Misc-difference 6
XX FT /note= "wild-type Asp5 is substd. by Lys"

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FT Region 14..40
FT /note= "helix 1"
FT Region 41..62
FT /note= "helix 2"
FT Region 63..95
FT /note= "helix 3"
FT Region 96..117
FT /note= "helix 4"
FT Region 118..139
FT /note= "helix 5"
FT Region 140..161
FT /note= "helix 6"
FT Region 162..183
FT /note= "helix 7"
FT Region 184..205
FT /note= "helix 8"
FT Region 206..227
FT /note= "helix 9"
FT Region 228..249
FT /note= "helix 10"
FT Region 250..267
FT /note= "helix 11"
FT Region 268..289
FT /note= "helix 12"
FT Region 290..311
FT /note= "helix 13"
FT Region 312..333
FT /note= "helix 14"
FT Region 334..377
FT /note= "helix 15"
XX WO9315198-A1.
XX PN
XX PD 05-AUG-1993.
XX PF 26-JAN-1993; 93WO-FR000073.
XX PR 27-JAN-1992; 92FR-00000806.
XX XX
XX PA (RHON ) RHONE POULENC RORER SA.
XX XX
XX PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX DR WPI; 1993-258676/32.
XX PF New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
FT FT and/or treatment of hypercholesterolaemia.
XX PS Claim 7; Page 31-32 and Page 5; 42pp; French.
XX CC Human apolipoprotein AIV is a major component of chylomicrons in lymph
CC but is mainly found in the plasma in unassociated form. The apo AIV
CC mediates inverse transport of cholesterol. The invention covers
CC polypeptides which are derived from apoAIV by deletion of at least 10
CC terminal amino acids, by deletion of a helix or pair of helices, by
CC addition of a heterologous polypeptide portion or by a point mutation.
CC Such muteins are useful in the design of hypocholesterolaemic drugs to
CC treat hypercholesterolaemia and atherosclerosis. AAR39502 is a
CC specifically claimed mutein and the sequence has been compiled from the
CC wild-type sequence (see AAR39443) and the description given in the
CC disclosure; the mutant sequence is not shown in the specification.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 377 AA;

Query Match 100.0%; Score 66; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 60 KLVPFATELHERL 72
|||||
|||||

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RESULT 25
 AAR39443
 ID AAR39443 standard; protein; 377 AA.
 XX AC AAR39443;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apolipoprotein AIV.
 XX
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 14..40
 FT /note= "helix 1"
 FT Region 41..62
 FT /note= "helix 2"
 FT Region 63..95
 FT /note= "helix 3"
 FT Region 96..117
 FT /note= "helix 4"
 FT Region 118..139
 FT /note= "helix 5"
 FT Region 140..161
 FT /note= "helix 6"
 FT Region 162..183
 FT /note= "helix 7"
 FT Region 184..205
 FT /note= "helix 8"
 FT Region 206..227
 FT /note= "helix 9"
 FT Region 228..249
 FT /note= "helix 10"
 FT Region 250..267
 FT /note= "helix 11"
 FT Region 268..289
 FT /note= "helix 12"
 FT Region 290..311
 FT /note= "helix 13"
 FT Region 312..333
 FT /note= "helix 14"
 FT Region 334..377
 FT /note= "helix 15"
 XX
 FN WO9315198-A1.
 XX
 PD 05-AUG-1993.
 XX
 XX 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 PR
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelier A;
 PI
 XX WPI; 1993-258676/32.
 DR N-PSDB; AAQ43306.
 XX
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
 XX and/or treatment of hypercholesterolaemia.
 PT
 XX Disclosure; Page 32-33; 42pp; French.
 PS
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apo AIV
 CC mediates inverse transport of cholesterol. The invention covers

polypeptides which are derived from apoAIV by deletion of at least 10
 terminal amino acids, by deletion of a helix or pair of helices, by
 addition of a heterologous polypeptide portion or by a point mutation.
 Such muteins are useful in the design of hypocholesterolaemic drugs to
 treat hypercholesterolaemia and atherosclerosis. (Updated on 25-MAR-2003
 to correct FN field.)
 XX
 SQ Sequence 377 AA;
 Query Match 100.0%; Score 66; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVPPFATELHERL 13
 |||||
 DB 60 KLVPPFATELHERL 72
 RESULT 26
 AAR45244
 ID AAR45244 standard; protein; 377 AA.
 XX AC AAR45244;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apoAIV mutein P(E230K).
 XX
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Protein 2..377
 FT /note= "mature P(E230K)"
 FT Region 14..40
 FT /note= "helix 1"
 FT Region 41..62
 FT /note= "helix 2"
 FT Region 63..95
 FT /note= "helix 3"
 FT Region 96..117
 FT /note= "helix 4"
 FT Region 118..139
 FT /note= "helix 5"
 FT Region 140..161
 FT /note= "helix 6"
 FT Region 162..183
 FT /note= "helix 7"
 FT Region 184..205
 FT /note= "helix 8"
 FT Region 206..227
 FT /note= "helix 9"
 FT Region 228..249
 FT /note= "helix 10"
 FT Misc-difference 231
 FT /note= "wild-type Glu230 is substd. by Lys"
 FT Region 250..267
 FT /note= "helix 11"
 FT Region 268..289
 FT /note= "helix 12"
 FT Region 290..311
 FT /note= "helix 13"
 FT Region 312..333
 FT /note= "helix 14"
 FT Region 334..377
 FT /note= "helix 15"
 XX
 FN WO9315198-A1.

```

PD 05-AUG-1993.
XX
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92FR-00000806.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX and/or treatment of hypercholesterolaemia.
XX
XX Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apo AIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such muteins are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR45243 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 377 AA;
XX
XX Query Match 100.0%; Score 66; DB 2; Length 377;
XX Best Local Similarity 100.0%; Pred. No. 0.00089;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Caps 0;
XX
XX QY 1 KLVPPFATLHERL 13
XX |||||
XX 60 KLVPPFATLHERL 72
XX
XX RESULT 27
XX AAR39501
XX ID AAR39501 standard; protein; 377 AA.
XX
XX AC AAR39501;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX
XX DE Human apoAIV mutein P(D5S).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecithin-cholesterol-acyltransferase; LCAT.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Protein 2..377
XX
XX Misc-difference 6
XX /note= "mature P(D5S)"
XX
XX Region 14..40
XX /note= "helix 1"
XX
XX Region 41..62
XX /note= "helix 2"
XX
XX Region 63..95
XX /note= "helix 3"
XX
XX Region 96..117
XX /note= "helix 4"
XX
XX Region 118..139
XX /note= "helix 5"
XX

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FT Region 140..161
FT /note= "helix 6"
FT Region 162..183
FT /note= "helix 7"
FT Region 184..205
FT /note= "helix 8"
FT Region 206..227
FT /note= "helix 9"
FT Region 228..249
FT /note= "helix 10"
FT Region 250..267
FT /note= "helix 11"
FT Region 268..289
FT /note= "helix 12"
FT Region 290..311
FT /note= "helix 13"
FT Region 312..333
FT /note= "helix 14"
FT Region 334..377
FT /note= "helix 15"
XX
XX W09315198-AI.
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92FR-00000806.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX and/or treatment of hypercholesterolaemia.
XX
XX Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apo AIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such muteins are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR39501 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 377 AA;
XX
XX Query Match 100.0%; Score 66; DB 2; Length 377;
XX Best Local Similarity 100.0%; Pred. No. 0.00089;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Caps 0;
XX
XX QY 1 KLVPPFATLHERL 13
XX |||||
XX 60 KLVPPFATLHERL 72
XX
XX RESULT 28
XX AAR45242
XX ID AAR45242 standard; protein; 377 AA.
XX
XX AC AAR45242;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX

```


Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 60 KLVPFATELHERL 72

RESULT 30
AAR39499
ID AAR39499 standard; protein; 377 AA.
XX
AC AAR39499;
XX
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1994 (first entry)
XX
DE Human apoAIV mutein P(D44F).
XX
KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
KW lecithin-cholesterol-acyltransferase; LCAT.
XX
OS Synthetic.

Key Location/Qualifiers
FT Protein 2..377
FT /note= "mature P(D44F)"
FT Region 14..40
FT /note= "helix 1"
FT Region 41..62
FT /note= "helix 2"
FT Misc-difference 45
FT /note= "wild-type Asp44 is substd. by Phe"
FT Region 63..95
FT /note= "helix 3"
FT Region 96..117
FT /note= "helix 4"
FT Region 118..139
FT /note= "helix 5"
FT Region 140..161
FT /note= "helix 6"
FT Region 162..183
FT /note= "helix 7"
FT Region 184..205
FT /note= "helix 8"
FT Region 206..227
FT /note= "helix 9"
FT Region 228..249
FT /note= "helix 10"
FT Region 250..267
FT /note= "helix 11"
FT Region 268..289
FT /note= "helix 12"
FT Region 290..311
FT /note= "helix 13"
FT Region 312..333
FT /note= "helix 14"
FT Region 334..377
FT /note= "helix 15"

XX WO9315198-A1.
XX
XX
PD 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92FR-0000806.
XX (RHON) RHONE POULENC RORER SA.
XX
XX Deneffe P, Guinet F, Latta M, Murry-Brelrier A;
XX WPI; 1993-259676/32.

XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug design
PT and/or treatment of hypercholesterolaemia.
XX
PS Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
CC Human apolipoprotein AIV is a major component of chylomicrons in lymph
CC but is mainly found in the plasma in unassociated form. The apo AIV
CC mediates inverse transport of cholesterol. The invention covers
CC polypeptides which are derived from apoAIV by deletion of at least 10
CC terminal amino acids, by deletion of a helix or pair of helices, by
CC addition of a heterologous polypeptide portion or by a point mutation.
CC Such muteins are useful in the design of hypocholesterolaemic drugs to
CC treat hypercholesterolaemia and atherosclerosis. AAR39499 is a
CC specifically claimed mutein and the sequence has been compiled from the
CC wild-type sequence (see AAR39443) and the description given in the
CC disclosure; the mutant sequence is not shown in the specification.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 377 AA;
Query Match 100.0%; Score 66; DB 2; Length 377;
Best Local Similarity 100.0%; Pred No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
Db 60 KLVPFATELHERL 72

RESULT 31
AAR39500
ID AAR39500 standard; protein; 377 AA.
XX
AC AAR39500;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1994 (first entry)
XX
DE Human apoAIV mutein P(D44A).
XX
KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
KW lecithin-cholesterol-acyltransferase; LCAT.
XX
OS Synthetic.

Key Location/Qualifiers
FT Protein 2..377
FT /note= "mature P(D44A)"
FT Region 14..40
FT /note= "helix 1"
FT Region 41..62
FT /note= "helix 2"
FT Misc-difference 45
FT /note= "wild-type Asp44 is substd. by Ala"
FT Region 63..95
FT /note= "helix 3"
FT Region 96..117
FT /note= "helix 4"
FT Region 118..139
FT /note= "helix 5"
FT Region 140..161
FT /note= "helix 6"
FT Region 162..183
FT /note= "helix 7"
FT Region 184..205
FT /note= "helix 8"
FT Region 206..227
FT /note= "helix 9"
FT Region 228..249
FT /note= "helix 10"
FT Region 250..267

FT Region /note= "helix 11"
 FT 268..289
 FT /note= "helix 12"
 FT 290..311
 FT /note= "helix 13"
 FT 312..333
 FT /note= "helix 14"
 FT 334..377
 FT /note= "helix 15"
 XX
 PN WO9315198-A1.
 XX
 XX 05-AUG-1993.
 PD
 XX 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 PA
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 PI
 XX WPI; 1993-258676/32.
 DR
 XX
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 PT
 XX
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 PS
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apo AIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39500 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 377 AA;

Query Match 100.0%; Score 66; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13
 Db 60 KLVPFATELHERL 72

RESULT 32
 AAR45243
 ID AAR45243 standard; protein; 377 AA.
 XX
 AC AAR45243;
 XX
 XX 25-MAR-2003 (revised)
 DT 28-JAN-1994 (first entry)
 DT
 XX Human apoAIV mutein P(K178A).
 DE
 XX
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;
 KW lecithin-cholesterol-acyltransferase; LCAT.
 XX
 XX Synthetic.

Key Location/Qualifiers
 FT Protein 2..377
 FT /note= "mature P(K178A)"
 FT

FT Region 14..40
 FT /note= "helix 1"
 FT 41..62
 FT /note= "helix 2"
 FT 63..95
 FT /note= "helix 3"
 FT 96..117
 FT /note= "helix 4"
 FT 118..139
 FT /note= "helix 5"
 FT 140..161
 FT /note= "helix 6"
 FT 162..183
 FT /note= "helix 7"
 FT Misc-difference 179
 FT /note= "wild-type Lys178 is substd. by Ala"
 FT 184..205
 FT /note= "helix 8"
 FT 206..227
 FT /note= "helix 9"
 FT 228..249
 FT /note= "helix 10"
 FT 250..267
 FT /note= "helix 11"
 FT 268..289
 FT /note= "helix 12"
 FT 290..311
 FT /note= "helix 13"
 FT 312..333
 FT /note= "helix 14"
 FT 334..377
 FT /note= "helix 15"
 FT
 FT WO9315198-A1.
 XX
 XX 05-AUG-1993.
 PD
 XX 26-JAN-1993; 93WO-FR0000073.
 XX
 XX 27-JAN-1992; 92FR-00000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 PA
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 PI
 XX WPI; 1993-258676/32.
 DR
 XX
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
 PT and/or treatment of hypercholesterolaemia.
 PT
 XX
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.
 PS
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
 CC but is mainly found in the plasma in unassociated form. The apo AIV
 CC mediates inverse transport of cholesterol. The invention covers
 CC polypeptides which are derived from apoAIV by deletion of at least 10
 CC terminal amino acids, by deletion of a helix or pair of helices, by
 CC addition of a heterologous polypeptide portion or by a point mutation.
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to
 CC treat hypercholesterolaemia and atherosclerosis. AAR39500 is a
 CC specifically claimed mutein and the sequence has been compiled from the
 CC wild-type sequence (see AAR39443) and the description given in the
 CC disclosure; the mutant sequence is not shown in the specification.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 377 AA;

Qy 1 KLVPFATELHERL 13

Db 60 KLVPFATELHERL 72

Query Match 100.0%; Score 66; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPFATELHERL 13

Query Match 100.0%; Score 66; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00089;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db      60 KLVPPFATELHERL 72

RESULT 33
AAB90663
ID AAB90663 standard; protein; 382 AA.
XX
AC AAB90663;
XX
XX 01-JUN-2001 (first entry)
DT
DE Human secreted protein, SEQ ID NO: 206.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; dermatological;
KW antiinflammatory; anti-HIV; cytostatic; cardiant; vascular;
KW anti-angiogenic; ophthalmological; neuroprotectant; neurotropic;
KW anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial;
KW vulnery; vaccine; gene therapy; cancer; protein coordinate data;
KW infection.
XX
XX Homo sapiens.
OS
XX WO200121658-A1.
XX
XX 29-MAR-2001.
XX
XX 22-SEP-2000; 2000WO-US026013.
XX
XX 24-SEP-1999; 99US-0155709P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Baker KP, Birse CE, Ebner R, Fiscella M, Komatsoulis GA;
PI Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;
PI Young PE, Wei P, Florence KA;
XX
XX WPI; 2001-235311/24.
XX
XX Nucleic acids encoding 32 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
PT and diabetic retinopathy.
XX
XX Disclosure; Page 869-870; 890pp; English.
XX
XX The present sequence is provided in a specification relating to nucleic
CC acid molecules encoding 32 novel human secreted polypeptides. The nucleic
CC acid molecules and polypeptides may be used in the prevention, diagnosis
CC and treatment of diseases such as immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immuno-deficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. The nucleic
CC acid molecules may be used to produce the secreted polypeptides. They may
CC also be used as DNA probes in diagnostic assays to detect and quantitate
CC the presence of similar nucleic acid sequences in samples. The
CC polypeptides may be used as antigens in the production of antibodies and
CC in assays to identify modulators of their expression and activity
XX
XX Sequence 382 AA;
XX
Query Match 100.0%; Score 66; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 79 KLVPPFATELHERL 91

RESULT 34
AAB90664
ID AAB90664 standard; protein; 396 AA.
XX
AC AAB90664;
XX
XX 01-JUN-2001 (first entry)
DT
DE Human secreted protein, SEQ ID NO: 207.
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; dermatological;
KW antiinflammatory; anti-HIV; cytostatic; cardiant; vascular;
KW anti-angiogenic; ophthalmological; neuroprotectant; neurotropic;
KW anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial;
KW vulnery; vaccine; gene therapy; cancer; protein coordinate data;
KW infection.
XX
XX Homo sapiens.
OS
XX WO200121658-A1.
XX
XX 29-MAR-2001.
XX
XX 22-SEP-2000; 2000WO-US026013.
XX
XX 24-SEP-1999; 99US-0155709P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Baker KP, Birse CE, Ebner R, Fiscella M, Komatsoulis GA;
PI Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;
PI Young PE, Wei P, Florence KA;
XX
XX WPI; 2001-235311/24.
XX
XX Nucleic acids encoding 32 human secreted polypeptides, useful for
PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease
PT and diabetic retinopathy.
XX
XX Disclosure; Page 870-871; 890pp; English.
XX
XX The present sequence is provided in a specification relating to nucleic
CC acid molecules encoding 32 novel human secreted polypeptides. The nucleic
CC acid molecules and polypeptides may be used in the prevention, diagnosis
CC and treatment of diseases such as immune disorders (e.g. multiple
CC sclerosis, systemic lupus erythematosus and human immuno-deficiency virus
CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
CC disorders (e.g. corneal graft neovascularisation and diabetic
CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis. The nucleic
CC acid molecules may be used to produce the secreted polypeptides. They may
CC also be used as DNA probes in diagnostic assays to detect and quantitate
CC the presence of similar nucleic acid sequences in samples. The
CC polypeptides may be used as antigens in the production of antibodies and
CC in assays to identify modulators of their expression and activity
XX
XX Sequence 396 AA;
XX
Query Match 100.0%; Score 66; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
DB 79 KLVPPFATELHERL 91

RESULT 35
AAB15885
ID AAB15885 standard; protein; 396 AA.

```

XX AAO15885;
 XX AC
 XX DT
 XX DE
 XX DE 30-JAN-2003 (first entry)
 XX DE Human apolipoprotein A-IV (APOA4).
 XX KW Human; gene therapy; single nucleotide polymorphism; SNP;
 XX KW cytochrome C oxidase subunit VIB; COX6B; high serum cholesterol; GPI-1;
 XX KW N-acetylglucosaminyl transferase component; cardiovascular disease; HDL;
 XX KW glycosylphosphatidylinositol-1; low serum high density lipoprotein.
 XX OS Homo sapiens.
 XX XX WO200272604-A2.
 XX XX 19-SEP-2002.
 XX XX 05-MAR-2002; 2002WO-US006728.
 XX XX 09-MAR-2001; 2001US-00802640.
 XX XX (SEQU-) SEQUENOM INC.
 XX XX Braun A, Bansal A, Kleyl PW;
 XX XX WPI; 2002-750478/81.
 XX XX N-PSDB; ABT13007.
 XX XX
 XX PT Detecting the presence or absence of an allelic variant of a polymorphic
 XX PT region of COX6B and/or GPI-1 gene, useful for detecting a predisposition
 XX PT to high serum cholesterol, low serum HDL and cardiovascular disease.
 XX XX
 XX PS Disclosure; Page 117; 199pp; English.
 XX CC The invention comprises methods of detecting the presence or absence of
 CC at least one allelic variant of a polymorphic region of a gene associated
 CC with cardiovascular disease. The invention specifically relates to
 CC detecting the region of a cytochrome C oxidase subunit VIB (COX6B) gene
 CC that is associated with high serum cholesterol, or the region of the N-
 CC acetylglucosaminyl transferase component glycosylphosphatidylinositol-1
 CC (GPI-1) gene that is associated with low serum high density lipoprotein
 CC (HDL). The methods of the invention are useful for detecting a
 CC predisposition to high serum cholesterol, low serum HDL and
 CC cardiovascular disease. The methods are also useful for elucidating
 CC pathological pathways, developing diagnostic assays and new drug
 CC therapies for such disorders. The present amino acid sequence represents
 CC a human protein that is associated with high serum cholesterol, low serum
 CC HDL and/or cardiovascular disease
 XX SQ Sequence 396 AA;
 Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVPFATLHERL 13
 Db 79 KLVPFATLHERL 91
 RESULT 36
 AAU10862
 ID AAU10862 standard; protein; 396 AA.
 XX AC
 XX AC AAU10862;
 XX DT 14-FEB-2002 (first entry)
 XX DE Human apolipoprotein A-IV, APOA4, isoform #2.
 XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;

XX atherosclerosis.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 111 /note= "Wild-type Ala substituted by Val"
 XX WO200177124-A2.
 XX PN 18-OCT-2001.
 XX PD 03-APR-2001; 2001WO-US010670.
 XX PF 05-APR-2000; 2000US-0194362P.
 XX PR (GENA-) GENAISSANCE PHARM INC.
 XX PA Bentivegna SC, Choi JY, Klem SE, Koshy B;
 XX PI WPI; 2002-041281/05.
 XX DR New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 XX PS Claim 29; Page; 71pp; English.
 XX CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3
 XX SQ Sequence 396 AA;
 Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLVPFATLHERL 13
 Db 79 KLVPFATLHERL 91
 RESULT 37
 AAU10863
 ID AAU10863 standard; protein; 396 AA.
 XX AC
 XX AC AAU10863;
 XX DT 14-FEB-2002 (first entry)
 XX DE Human apolipoprotein A-IV, APOA4, isoform #3.
 XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 127

PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;
 XX WPI; 2002-041281/05.
 XX
 XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 XX
 XX Claim 29; Page; 71pp; English.
 XX
 XX The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3
 XX
 SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. NO. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 DB 79 KLVPPFATELHERL 91

RESULT 40
 AAU10866
 ID AAU10866 standard; protein; 396 AA.
 AC
 XX AAU10866;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 XX Human apolipoprotein A-IV, APOA4, isoform #6.
 DE
 XX Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 193
 FT /label= Met, Ile
 FT /note= "replaces wild-type Val"
 XX
 XX WO200177124-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 03-APR-2001; 2001WO-US010670.
 XX
 XX 05-APR-2000; 2000US-0194362P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;
 XX WPI; 2002-041281/05.
 XX
 XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose

PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 XX
 XX Claim 29; Page; 71pp; English.
 XX
 XX The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3
 XX
 SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. NO. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 DB 79 KLVPPFATELHERL 91

RESULT 41
 AAU10869
 ID AAU10869 standard; protein; 396 AA.
 AC
 XX AAU10869;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 XX Human apolipoprotein A-IV, APOA4, isoform #9.
 DE
 XX Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 380
 FT /note= "Wild-type His substituted by Gln"
 FT
 XX WO200177124-A2.
 XX
 XX 18-OCT-2001.
 XX
 XX 03-APR-2001; 2001WO-US010670.
 XX
 XX 05-APR-2000; 2000US-0194362P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;
 XX WPI; 2002-041281/05.
 XX
 XX New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 XX
 XX Claim 29; Page; 71pp; English.
 XX
 XX The invention relates to haplotyping the human apolipoprotein A-IV

CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 DB 79 KLVPPFATELHERL 91
 |||||

RESULT 42
 AAU10861
 ID AAU10861 standard; protein; 396 AA.

XX AC AAU10861;

XX DT 14-FEB-2002 (first entry)

XX DE Human apolipoprotein A-IV, APOA4, isoform #1.

XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 13 /note= "Wild-type Val substituted by Met"

XX FT WO20017124-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010670.

XX PR 05-APR-2000; 2000US-0194362P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;

XX DR WPI; 2002-041281/05.

XX PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.

XX PS Claim 29; Page; 71pp; English.

XX CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the

CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 DB 79 KLVPPFATELHERL 91
 |||||

RESULT 43

AAU10868
 ID AAU10868 standard; protein; 396 AA.

XX AC AAU10868;

XX DT 14-FEB-2002 (first entry)

XX DE Human apolipoprotein A-IV, APOA4, isoform #8.

XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 367 /note= "Wild-type Thr substituted by Ser"

XX FT WO20017124-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010670.

XX PR 05-APR-2000; 2000US-0194362P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;

XX DR WPI; 2002-041281/05.

XX PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.

XX PS Claim 29; Page; 71pp; English.

XX CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:

CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
 |||||
 Db 79 KLVPPFATLHERL 91

RESULT 44
 AAU10860
 ID AAU10860 standard; protein; 396 AA.

XX AC AAU10860;

DT 14-FEB-2002 (first entry)

XX DE Human apolipoprotein A-IV, APOA4.

XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.

XX OS Homo sapiens.

XX PN WO200177124-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010670.

XX PR 05-APR-2000; 2000US-0194362P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;

XX DR WPI; 2002-041281/05.

XX DR N-PSDB; AAS16512, AAS16513.

XX PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.

XX PS Claim 29; Fig 3; 71pp; English.

XX CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is the APOA4 protein

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
 |||||

Db 79 KLVPPFATLHERL 91

RESULT 45

AAU10864

ID AAU10864 standard; protein; 396 AA.

XX AC AAU10864;

DT 14-FEB-2002 (first entry)

XX DE Human apolipoprotein A-IV, APOA4, isoform #4.

XX KW Human; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 147

XX FT /note= "Wild-type Asn substituted by Ser"

XX PN WO200177124-A2.

XX PD 18-OCT-2001.

XX PF 03-APR-2001; 2001WO-US010670.

XX PR 05-APR-2000; 2000US-0194362P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;

XX DR WPI; 2002-041281/05.

XX PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.

XX PS Claim 29; Page; 71pp; English.

XX CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an isoform of the APOA4 protein. Note:
 CC The present sequence is not shown in the specification but was created by
 CC the indexer from the APOA4 sequence shown in figure 3

XX SQ Sequence 396 AA;

Query Match 100.0%; Score 66; DB 5; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.00094;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVPPFATLHERL 13
 |||||

Db 79 KLVPPFATLHERL 91

Search completed: September 1, 2005, 16:37:42
 Job time : 170 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 16:21:35 ; Search time 174 Seconds
(without alignments)
38.259 Million cell updates/sec

Title: US-09-993-366-1

Perfect score: 66

Sequence: 1 KLVPFATELHERL 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	102	2	Q29258
2	66	100.0	382	1	Q29258 sus scrofa
3	66	100.0	382	1	Q29258 sus scrofa
4	66	100.0	401	1	Q29258 sus scrofa
5	66	100.0	429	1	Q29258 sus scrofa
6	45	68.2	366	1	Q29258 sus scrofa
7	42	63.6	436	1	Q29258 sus scrofa
8	42	63.6	434	2	Q29258 sus scrofa
9	42	63.6	437	2	Q29258 sus scrofa
10	41	62.1	258	2	Q29258 sus scrofa
11	41	62.1	258	2	Q29258 sus scrofa
12	41	62.1	261	2	Q29258 sus scrofa
13	41	62.1	265	2	Q29258 sus scrofa
14	41	62.1	367	2	Q29258 sus scrofa
15	41	62.1	897	2	Q29258 sus scrofa
16	41	62.1	1056	2	Q29258 sus scrofa
17	41	62.1	1179	2	Q29258 sus scrofa
18	40	60.6	260	1	Q29258 sus scrofa
19	40	60.6	266	1	Q29258 sus scrofa
20	40	60.6	368	2	Q29258 sus scrofa
21	40	60.6	585	2	Q29258 sus scrofa
22	40	60.6	656	2	Q29258 sus scrofa
23	39	59.1	150	2	Q29258 sus scrofa
24	39	59.1	177	2	Q29258 sus scrofa
25	39	59.1	220	2	Q29258 sus scrofa
26	39	59.1	353	2	Q29258 sus scrofa
27	39	59.1	697	2	Q29258 sus scrofa
28	39	59.1	2710	2	Q29258 sus scrofa
29	39	59.1	2796	2	Q29258 sus scrofa
30	39	59.1	3069	2	Q29258 sus scrofa
31	39	59.1	3069	2	Q29258 sus scrofa

ALIGNMENTS

32	39	59.1	3069	2	Q7TYD8	Q7tyd8 mycobacteri
33	39	59.1	3076	2	Q9X7E2	Q9x7e2 mycobacteri
34	39	59.1	3092	2	Q73XH7	Q73xh7 mycobacteri
35	38	57.6	57	2	Q6K305	Q6k305 oryza sativ
36	38	57.6	162	2	Q89SR9	Q89sr9 bradyrhizob
37	38	57.6	176	2	Q6HCP9	Q6hcp9 bacillus th
38	38	57.6	250	2	Q9X548	Q9x548 corynebacte
39	38	57.6	288	2	Q33624	Q33624 streptomyce
40	38	57.6	311	2	Q6GK71	Q6gk71 staphylococ
41	38	57.6	314	2	Q6RWS4	Q6rws4 uncultured
42	38	57.6	317	2	Q6G538	Q6g538 aquifex aeo
43	38	57.6	319	2	Q8TYA1	Q8tya1 methanopyru
44	38	57.6	330	2	Q67L63	Q67l63 symbiobacte
45	38	57.6	335	2	Q6R3I5	Q6r3i5 gemmata sp.
46	38	57.6	354	2	Q8FC11	Q8fc11 escherichia
47	38	57.6	391	1	Q891C2	Q891c2 clostridium
48	38	57.6	394	1	Q891C2	Q891c2 clostridium
49	38	57.6	405	1	Q891C2	Q891c2 clostridium
50	38	57.6	423	2	Q75TW9	Q75tw9 bacillus ha
51	38	57.6	428	1	Q75TW9	Q75tw9 bacillus ha
52	38	57.6	429	1	PURA_BACHD	Pura_BACHD
53	38	57.6	429	1	PURA_BACAN	Pura_BACAN
54	38	57.6	429	1	PURA_BACCR	Pura_BACCR
55	38	57.6	429	1	PURA_OCEIH	Pura_OCEIH
56	38	57.6	429	2	Q630D5	Q630d5 bacillus ce
57	38	57.6	429	2	Q72MW1	Q72mw1 bacillus ce
58	38	57.6	432	1	Q6HAG9	Q6hag9 bacillus th
59	38	57.6	432	1	PURA_AGR75	Pura_AGR75
60	38	57.6	472	1	Q7SA_SALTY	Q7sa_salty
61	38	57.6	474	2	Q7BJX2	Q7bjx2 plasmodium
62	38	57.6	543	2	Q28264	Q28264 archaeoglob
63	38	57.6	589	2	Q83989	Q83989 treponema p
64	38	57.6	652	2	Q82C93	Q82c93 streptomyce
65	38	57.6	661	2	Q9L1H1	Q9l1h1 streptomyce
66	38	57.6	669	1	HPO_DROME	Hpo_DROME
67	38	57.6	711	2	Q8D4D6	Q8d4d6 drosophila
68	38	57.6	715	2	Q7MFW4	Q7mfw4 vibrio vuln
69	38	57.6	847	1	Q9SLU4	Q9slu4 arabidopsis
70	38	57.6	849	1	RS62_HUMAN	Rs62_HUMAN
71	38	57.6	864	1	Q6YOR8	Q6yor8 onion yello
72	38	57.6	864	1	GCSP_ANASP	Gcsp_ANASP
73	38	57.6	987	1	TNPA_BACTU	Tnpa_BACTU
74	38	57.6	1330	2	Q9SXQ2	Q9sxq2 arabidopsis
75	38	57.6	1421	2	Q9SXQ2	Q9sxq2 arabidopsis
76	38	57.6	1431	2	Q9SXQ1	Q9sxq1 arabidopsis
77	38	57.6	1447	2	Q9SXQ3	Q9sxq3 arabidopsis
78	38	57.6	1456	2	Q9ZT94	Q9zt94 arabidopsis
79	38	57.6	1459	2	Q94LA8	Q94la8 arabidopsis
80	38	57.6	1466	2	Q94HM2	Q94hw2 arabidopsis
81	38	57.6	1466	2	Q94HM2	Q94hw2 arabidopsis
82	38	57.6	1474	2	Q23529	Q23529 arabidopsis
83	38	57.6	1475	2	Q9SXQ4	Q9sxq4 arabidopsis
84	38	57.6	1592	2	Q8U110	Q8j110 cryptococcu
85	38	57.6	1593	2	Q8U0X4	Q8j0x4 cryptococcu
86	38	57.6	4600	2	Q8IF9	Q8iff9 trypanosoma
87	37	56.1	95	2	Q7PLK4	Q7plk4 drosophila
88	37	56.1	100	2	Q50146	Q50146 mycobacteri
89	37	56.1	147	2	Q8L1J3	Q8l1j3 clostridium
90	37	56.1	176	2	Q63LD3	Q63ld3 burkholderi
91	37	56.1	209	2	Q8GMR9	Q8gm9 synecococc
92	37	56.1	222	2	Q9XX17	Q9xx17 caenorhabdi
93	37	56.1	226	2	Q7Q041	Q7q041 anopheles g
94	37	56.1	259	1	APAL_RAT	P04639 rattus norv
95	37	56.1	263	2	Q70C4	Q70cc4 eimeria ten
96	37	56.1	263	1	APAL_PIG	P18648 sus scrofa
97	37	56.1	268	2	Q70CD2	Q70cd2 eimeria ten
98	37	56.1	270	2	Q70CD3	Q70cd3 eimeria ten
99	37	56.1	279	2	Q72TT1	Q72tt1 leptospira
100	37	56.1	279	2	Q8F1E4	Q8f1e4 leptospira

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EMBL; AJ222966; CAA11020.1; --
HSSP; P32851; 1E23.
DR InterPro; IPR009074; Apolipo_A_E_C3.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Chylomicron; HDL; Lipid transport; Plasma; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 382
FT DOMAIN 33 330
FT REPEAT 33 54
FT REPEAT 60 81
FT REPEAT 82 103
FT REPEAT 115 136
FT REPEAT 137 158
FT REPEAT 159 180
FT REPEAT 181 202
FT REPEAT 203 224
FT REPEAT 225 246
FT REPEAT 247 268
FT REPEAT 269 286
FT REPEAT 287 308
FT REPEAT 309 330
FT DOMAIN 360 377
SQ SEQUENCE 382 AA; 43294 MW; 2ACA88A02D4379EF CRC64;
Query Match 100.0%; Score 66; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVPFATLHERL 13
DB 79 KLVPFATLHERL 91

RESULT 3
APA4 HUMAN
ID _APA4 HUMAN STANDARD; PRT; 396 AA.
AC P06727;
DT 01-JAN-1988 (Rel. 06, Created)
DD 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN Name=APOA4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=87041474; PubMed=3095836;
RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
RA Gotto A.M. Jr., Chan L.;
RT "The primary structure of human apolipoprotein A-IV.";
RL Biochim. Biophys. Acta 1002:231-237(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87041474; PubMed=3095836;
RT Karathanasis S.K., Oettgen P., Haddad I.A., Antonarakis S.E.;
RT "Structure, evolution, and polymorphisms of the human apolipoprotein
RT A4 gene (APOA4).";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86296629; PubMed=3755616;

RESULT 1
 Q29258
 ID Q29258 PRELIMINARY; PRT; 102 AA.
 AC Q29258;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Apolipoprotein A-IV (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine cDNA
 RT library.";
 RL Mamm. Genome 7:509-517(1996).
 DR EMBL; F14546; CAA23119.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR GO; GO:0006869; P:lipid transport; IEA.
 DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
 DR InterPro; IPR000074; Apolipoprotein.
 DR InterPro; IPR009074; Apolipo_A_E_C3.
 DR Pfam; PF01442; Apolipoprotein; 1.
 DR Lipoprotein.
 FT NON TER 102 102
 SQ SEQUENCE 102 AA; 11534 MW; 123EAEEL134FBC8A CRC64;

 Query Match 100.0%; Score 66; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 0.00065;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KLVPFATLHERL 13
 DB 79 KLVPFATLHERL 91

 RESULT 2
 AF04_PIG
 ID AF04_PIG STANDARD; PRT; 382 AA.
 AC 046409;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN Name=APOA4;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osada J., Iturralde M., Calleja L., Gonzalez N., Pineseiro A.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and
 CC catabolism. Required for efficient activation of lipoprotein
 CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major
 CC component of HDL and chylomicrons.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Secreted in plasma.
 CC -!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each
 CC 22-mer is actually a tandem array of two, A and B, related 11-
 CC mers) occurring in this sequence are predicted to be highly alpha-
 CC helical, and many of these helices are predicted to be highly alpha-
 CC therefore serve as lipid-binding domains with lecithin:cholesterol
 CC acyltransferase (LCAT) activating abilities.
 CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

RA Karathanasis S.K., Yunis I.;
 RT "Structure, evolution, and tissue-specific synthesis of human
 RT apolipoprotein AIV.";
 RL Biochemistry 25:3962-3970(1986).
 [4]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87250378; PubMed=3036793;
 RX Elshourbagy N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,
 RA Gordon J.I., Taylor J.M.;
 RT "Structure and expression of the human apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 262:7973-7981(1987).
 [5]
 RN SEQUENCE OF 21-396 FROM N.A.
 RP MEDLINE=86111895; PubMed=3080432;
 RX Elshourbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
 RA "The nucleotide and derived amino acid sequence of human
 RT apolipoprotein A-IV mRNA and the close linkage of its gene to the
 RT genes of apolipoproteins A-I and C-III.";
 RL J. Biol. Chem. 261:1998-2002(1986).
 [6]
 RN SIGNAL SEQUENCE CLEAVAGE SITE.
 RP MEDLINE=84161950; PubMed=6706947;
 RX Gordon J.I., Bisgaier C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
 RA Strauss A.W.;
 RT "Biosynthesis of human preapolipoprotein A-IV.";
 RL J. Biol. Chem. 259:468-474(1984).
 [7]
 RN REVIEW ON POLYMORPHISM.
 RP Lohse P., Brewer H.B. Jr.;
 RA "Genetic polymorphism of apolipoprotein A-IV.";
 RL Curr. Opin. Lipidol. 2:90-95(1991).
 [8]
 RN VARIANT A-IV*2.
 RP MEDLINE=90277616; PubMed=2351649;
 RX Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RA "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 RT nucleotide substitutions in the apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 265:10061-10064(1990).
 [9]
 RN VARIANTS A-IV*0 AND A-IV*3.
 RP MEDLINE=90324273; PubMed=1973689;
 RX Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RA "Human plasma apolipoproteins A-IV-0 and A-IV-3. Molecular basis for
 RT two rare variants of apolipoprotein A-IV-1.";
 RL J. Biol. Chem. 265:12734-12739(1990).
 [10]
 RN VARIANTS.
 RP MEDLINE=91310615; PubMed=1677358;
 RX Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RA "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 RT 1(Thr-347-->Ser), apoA-IV-0(Lys-167-->Glu,Gln-360-->His), and apoA-IV-
 RT 3(Glu-165-->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).
 [11]
 RN ERRATUM.
 RP Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RA J. Biol. Chem. 266:19866-19866(1991).
 [12]
 RN VARIANT MET-13.
 RP MEDLINE=92238494; PubMed=1349197;
 RX von Eckardstein A., Funke H., Schulte H., Erren M., Schulte H.,
 RA Asmann G.;
 RA "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV gene
 RT are associated with changes in the concentration of apo B- and apo A-
 RT I-containing lipoproteins in a normal population.";
 RL Am. J. Hum. Genet. 50:1115-1128(1992).
 [13]
 RN VARIANT SER-147.
 RP MEDLINE=92144647; PubMed=1737067; DOI=10.1016/0925-4439(92)90147-F;
 RX Tenkanen H., Koskenen P., Metsä J., Baumann M., Lukka M.,
 RA Kauppinen-Makelin R., Kontula K., Taskinen M.R., Manttari M.,
 RA Manninen V., Ehnholm C.;
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an

RT asparagine to serine substitution at residue 127.";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 [14]
 RN VARIANT A-IV*5.
 RP MEDLINE=93138374; PubMed=14871136;
 RX Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.;
 RA "Molecular basis of a unique African variant (A-IV 5) of human
 RT apolipoprotein A-IV and its significance in lipid metabolism.";
 RL Genet. Epidemiol. 9:379-388(1992).
 [15]
 RN VARIANTS BUDAPEST-2 LYS-44; BUDAPEST-1 CYS-305 AND SER-367.
 RP MEDLINE=95245341; PubMed=7728150;
 RX Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,
 RA Csaszar A.;
 RA "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RT frequencies, effect on lipid levels, and sequence of two new
 RT variants.";
 RL Hum. Mutat. 5:58-65(1995).
 [16]
 RN VARIANTS SEATTLE-3 SER-161; SEATTLE-1 LEU-178 AND SEATTLE-2 GLN-264.
 RP MEDLINE=97114287; PubMed=8956036;
 RX DOI=10.1002/(SICI)1098-1004(1996)8:4<319::AID-HUMU4>3.3.CO;2-T;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
 RA "Two novel apolipoprotein A-IV variants in individuals with familial
 RT combined hyperlipidemia and diminished levels of lipoprotein lipase
 RT activity.";
 RL Hum. Mutat. 8:319-325(1996).
 [17]
 RN VARIANT HIS-380.
 RP MEDLINE=99318094; PubMed=10391210; DOI=10.1038/10297;
 RX Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
 RA Cooper R., Lipshutz R., Chakravarti A.;
 RA "Patterns of single-nucleotide polymorphisms in candidate genes for
 RT blood-pressure homeostasis.";
 RL Nat. Genet. 22:239-247(1999).
 CC -I- FUNCTION: May have a role in chylomicrons and VLDL secretion and
 CC catabolism. Required for efficient activation of lipoprotein
 CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major
 CC component of HDL and chylomicrons.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Synthesized primarily in the intestine and
 CC secreted in plasma.
 CC -I- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each
 CC 22-mer is actually a tandem array of two, A and B, related 11-
 CC mers) occurring in this sequence are predicted to be highly alpha-
 CC helical, and many of these helices are amphipathic. They may
 CC therefore serve as lipid-binding domains with lecithin:cholesterol
 CC acyltransferase (LCAT) activating abilities.
 CC -I- POLYMORPHISM: Eight alleles have been characterized (APOA-IV*0 to
 CC APOA-IV*7). APOA-IV*1 is the major allele (90%), APOA-IV*2 is also
 CC common (8%), the others are rare alleles.
 CC -I- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
 CC
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 CC
 CC EMBL; M14642; AAA51745.1; -
 CC EMBL; X13629; CAA31955.1; -
 CC EMBL; M14566; AAA51748.1; -
 CC EMBL; J02758; AAA96731.1; -
 CC EMBL; M13654; AAA51744.1; -
 CC PIR; A94137; LPHU44.
 CC HSP; P02649; IOR2.
 CC SWISS-2DPAGE; P06727; HUMAN.
 CC Genew; HGNC:602; APOA4.
 CC MIM; 107690; -
 CC GO; GO:0005319; F:lipid transporter activity; TAS.

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DR GO: GO:0008015; P:circulation; TAS.
DR GO: GO:006869; P:lipid transport; TAS.
DR InterPro: IPR009074; Apolipo_A_E_C3.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam: PF01442; Apolipoprotein; 2.
KW Chylomicron; HDL; Lipid transport; Plasma; Polymorphism; Repeat;
Signal.
FT SIGNAL 1 20
FT CHAIN 21 396
FT DOMAIN 33 330
FT REPEAT 33 54
FT REPEAT 60 81
FT REPEAT 82 103
FT REPEAT 115 136
FT REPEAT 137 158
FT REPEAT 159 180
FT REPEAT 181 202
FT REPEAT 203 224
FT REPEAT 225 246
FT REPEAT 247 268
FT REPEAT 269 286
FT REPEAT 287 308
FT REPEAT 309 330
FT DOMAIN 372 389
FT VARIANT 13 13
Query Match 100.0%; Score 66; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 79 KLVPPFATLHERL 91

RESULT 4
APAA PAPAN STANDARD; PRT; 401 AA.
AC Q28756;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV) (Fragment).
GN Name=APOA4;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=93340170; PubMed=8101842;
RA Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,
RA Powers P.K., Vandeberg J.L.;
RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that
RT distinguishes two common isoforms and detection of length
RT polymorphisms at the carboxyl terminus.";
RL J. Biol. Chem. 268:15667-15673(1993).
CC -1- FUNCTION: May have a role in chylomicrons and VLDL secretion and
CC catabolism. Required for efficient activation of lipoprotein
CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major
CC component of HDL and chylomicrons.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized primarily in the intestine and
CC secreted in plasma.
CC -1- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each
CC 22-mer is actually a tandem array of two, A and B, related 11-
CC mers) occurring in this sequence are predicted to be highly alpha-
CC helical, and many of these helices are amphipathic. They may
CC therefore serve as lipid-binding domains with lecithin:cholesterol
CC acyltransferase (LCAT) activating abilities.
CC -1- POLYMORPHISM: There are two common APOA-IV isoforms, I (shown

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CC here) and E. The I isoform is associated with higher levels of
CC high density lipoprotein-C on a high cholesterol, saturated fat
CC diet.
CC -1- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L13174; AAA35379.1; -.
DR HSSP; P02649; 1B68.
DR InterPro: IPR009074; Apolipo_A_E_C3.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Chylomicron; HDL; Lipid transport; Plasma; Polymorphism; Repeat;
Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 401
FT DOMAIN 17 314
FT REPEAT 17 38
FT REPEAT 44 65
FT REPEAT 66 87
FT REPEAT 99 120
FT REPEAT 121 142
FT REPEAT 143 164
FT REPEAT 165 186
FT REPEAT 187 208
FT REPEAT 209 230
FT REPEAT 231 252
FT REPEAT 253 270
FT REPEAT 271 292
FT REPEAT 293 314
FT DOMAIN 356 394
FT VARIANT 80 80
SQ SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;
Query Match 100.0%; Score 66; DB 1; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
Db 63 KLVPPFATLHERL 75

RESULT 5
APAA MACFA STANDARD; PRT; 429 AA.
AC P33621;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN Name=APOA4;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=93192330; PubMed=8448212; DOI=10.1016/0167-4781(93)90226-4;
RA Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III
RT and A-IV genes.";
RL Biochim. Biophys. Acta 1172:335-339(1993).
CC -1- FUNCTION: May have a role in chylomicrons and VLDL secretion and

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DR Pfam; PF01366; DAO; 1.
DR PRINTS; PR00335; KUPATKETRKA.
KW Complete proteome; FAD; Flavoprotein; Oxidoreductase.
SQ NP_BIND 3 17 FAD (ADP part) (Potential).
FT SEQUENCE 436 AA; 47971 MW; 24216B33BF0B331C CRC64;

Query Match 63.6%; Score 42; DB 1; Length 436;
Best Local Similarity 61.5%; Pred. No. 59;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
DB 422 KLVPPFASHQLHTEL 434

RESULT 8
Q9VLA0 PRELIMINARY; PRT; 4345 AA.
AC Q9VLA0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG15828-PA.
GN ORFNames=CG15828;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li F.W., Hoskins R.A., Calle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=22426065; PubMed=12537568;

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RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
RP MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whittier E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003625; AAF52796.1; -.
DR FlyBase; Fggn0032136; CG15828.
DR GO; GO:0005319; Filippid transporter activity; IEA.
DR GO; GO:0006869; Filippid transport; IEA.
DR InterPro; IPR009454; DUF1081.
DR InterPro; IPR001747; Lipid transprt N.
DR InterPro; IPR011030; LV superhelical.
DR InterPro; IPR001846; VWF D.
DR Pfam; PF06448; DUF1081; 1.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR Pfam; PF00094; VMD; 1.
DR SMART; SM00638; LPD_N; 1.
DR SMART; SM00216; VMD; 1.
SQ SEQUENCE 4345 AA; 495238 MW; 30AAC8439A52165F CRC64;

Query Match 63.6%; Score 42; DB 2; Length 4345;
Best Local Similarity 69.2%; Pred. No. 6e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATLHERL 13
DB 3596 KLVPPFGAELNEVL 3608

RESULT 9
Q7KTG2 PRELIMINARY; PRT; 4374 AA.
ID Q7KTG2
AC Q7KTG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG15828-PB.
GN ORFNames=CG15828;
OS Drosophila melanogaster (Fruit fly).

```

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

[1]

RN SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwee R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Fodor K.J., Evangelista C.C., Ferraz C., Ferrier A.S., Fleischmann W.,
 RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nuskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*;"
 RL Science 287:2185-2195(2000).

[2]

RN SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun. Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence".
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

[3]

RN SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective".
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

[4]

RN SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bertram B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

[5]

RN SEQUENCE FROM N.A.
 RP FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AS003625; AAS64667.1; -;
 DR GO; GO:0005319; F.lipid transporter activity; IEA.
 DR GO; GO:0006869; P.lipid transport; IEA.
 DR InterPro; IPR009454; DUF1081.
 DR InterPro; IPR001747; Lipid_transprt_N.
 DR InterPro; IPR011030; LV_superhelical.
 DR InterPro; IPR001846; VWF_D.
 DR Pfam; PF06448; DUF1081; 1.
 DR Pfam; PF01347; Vitellogenin_N; 1.
 DR Pfam; PF00094; VWD; 1.
 DR SMART; SM00638; LPD_N; 1.
 DR SMART; SM00216; VWD; 1.
 DR SEQUENCE 4374 AA; 498710 MW; C13F0DB2453D0F95 CRC64;

Query Match 53.6%; Score 42; DB 2; Length 4374;
 Best Local Similarity 69.2%; Pred. No. 6e+02;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPFPAELHERL 13

Db 3625 KLVPFGAELNEVL 3637

RESULT 10

O08877 PRELIMINARY; PRT; 258 AA.
 ID O08877
 AC O08877; 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Apolipoprotein A-I.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SHR; TISSUE=Spleen;
 RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 RT gene";
 RL Biochem. Mol. Biol. Int. 43:989-996(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SHR; TISSUE=Spleen;
 RA Chiang A.-N., Fan K.-C., Shaw G.-C., Yang U.-C.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U75576; AAB58428.1; -;
 DR HSP; P02647; IAV1.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR GO; GO:0006869; P:lipid transport; IEA.
 DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
 DR InterPro; IPR000074; Apolipoprotein.
 DR InterPro; IPR009074; Apolipo_A_E_C3.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29831 MW; 093FB582E629CDC8 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 258;
 Best Local Similarity 72.7%; Pred. No. 53;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPFATLH 11
 ||| |||||
 Db 140 KLEPLATLHK 150

RESULT 11

ID O09054 PRELIMINARY; PRT; 258 AA.
 AC O09054;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Apolipoprotein A-I.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WKY, and SHRSP; TISSUE=Spleen;
 RX MEDLINE=98077648; PubMed=9415807;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RT "Repetitive elements in the third intron of murine apolipoprotein A-I
 gene.";
 RL Biochem. Mol. Biol. Int. 43:989-996 (1997).
 RN [2]

SEQUENCE FROM N.A.

RC STRAIN=WKY, and SHRSP; TISSUE=Spleen;
 RA Chiang A.N., Fan K.C., Shaw G.C., Yang U.C.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79578; AAB58430.1; -.
 DR EMBL; U79577; AAB58429.1; -.
 DR HSSP; P02647; 1AV1.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:000289; F:lipid binding; IEA.
 DR GO; GO:0006969; P:lipid transport; IEA.
 DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
 DR InterPro; IPR000074; Apolipoprotein.
 DR InterPro; IPR009074; Apolipo A E C3.
 DR Pfam; PF01442; Apolipoprotein; 1.
 KW Lipoprotein.
 SQ SEQUENCE 258 AA; 29918 MW; 09356EP2E629CDC8 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 258;
 Best Local Similarity 72.7%; Pred. No. 53;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPFATLH 11
 ||| |||||
 Db 140 KLEPLATLHK 150

RESULT 12

ID Q8U799 PRELIMINARY; PRT; 261 AA.
 AC Q8U799;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein Atu4555.
 GN OrderedLocusNames=Atu4555;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;

RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eissen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Krespan W., Perry M.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323 (2001).
 DR EMBL; AB009383; AAL45349.1; -.
 DR PIR; AG3116; AG3116.
 DR PIR; F98170; F98170.
 DR Pfam; PF01261; AP_endonuc_2; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 261 AA; 27803 MW; 223234D33FE61D71 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 261;
 Best Local Similarity 87.5%; Pred. No. 54;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFATELHE 11
 |||||:
 Db 235 PFATEVHE 242

RESULT 13

ID Q7CV91 PRELIMINARY; PRT; 265 AA.
 AC Q7CV91;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE AGR L 627p.
 GN OrderedLocusNames=AGR L 627;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cereon;
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
 RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE008232; AAK88888.1; -.
 DR InterPro; IPR001719; AP_endonuclease2.
 DR Pfam; PF01261; AP_endonuc_2; 1.
 SQ SEQUENCE 265 AA; 28325 MW; 08895F05C995969B CRC64;

Query Match 62.1%; Score 41; DB 2; Length 265;
 Best Local Similarity 87.5%; Pred. No. 55;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PFATELHE 11
 |||||:
 Db 239 PFATEVHE 246

RESULT 14

Q6P7H6 PRELIMINARY; PRT; 367 AA.
 ID Q6P7H6

AC Q6P7H6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC68602 protein.
 GN Name=MGC68602;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TTSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TTSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.B., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TTSUE=Kidney;
 RA Klein S., Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC061667; AA61667.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR GO; GO:0006869; P:lipid transport; IEA.
 DR GO; GO:0042157; P:lipoprotein metabolism; IEA.
 DR InterPro; IPR000074; Apolipoprotein.
 DR InterPro; IPR009074; Apolipo_A_E_C3.
 DR Pfam; PF01442; Apolipoprotein; 2.
 SQ SEQUENCE 367 AA; 42332 MW; 699D578FE4626E78 CRC64;
 Query Match 62.1%; Score 41; DB 2; Length 367;
 Best Local Similarity 38.5%; Pred. No. 76;
 Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLVPFATLHERL 13
 DB 79 QLIPFAKQIHQDM 91
 RESULT 15
 Q89EW7 PRELIMINARY; PRT; 897 AA.
 AC Q89EW7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Molybdenum ABC transporter ATP-binding protein.
 GN Name=moaC; OrderedLocusNames=blr6953;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USD110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashina K.,
 RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL; AP005960; BAC52218.1; -
 DR HSSP; Q9YGA6; 1G29.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR InterPro; IPR008995; MOP_like.
 DR InterPro; IPR005116; TOBE.
 DR Pfam; PF00005; ABC_tran; 1.
 DR Pfam; PF03459; TOBE; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 897 AA; 96173 MW; 154C54F8D41A4D12 CRC64;
 Query Match 62.1%; Score 41; DB 2; Length 897;
 Best Local Similarity 53.8%; Pred. No. 1.9e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KLVPFATLHERL 13
 DB 173 EILPFLERLHERL 185
 RESULT 16
 Q7Q9K3 PRELIMINARY; PRT; 1056 AA.
 ID Q7Q9K3
 AC Q7Q9K3; (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AGCP15000 (Fragment).
 GN Name=agCG46168; ORFNames=ENSANGG00000007942;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Anopheles.
 NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAA01008900; EAA09356.1; -
 DR EMBL; AAA01008900; EAA09356.1; -
 FT NON_TER 1
 FT NON_TER 1056 1056

```

SQ SEQUENCE 1056 AA; 121746 MW; 191129F749BA27A2 CRC64;
Query Match 62.1%; Score 41; DB 2; Length 1056;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPFATELHERL 13
Db 61 KLQPFANKLQYL 73

RESULT 17
Q6NJ57 PRELIMINARY; PRT; 1179 AA.
AC Q6NJ57;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Putative FtsK/SpoIIIE family ATP-binding protein.
GN Ordered locus names=DIP0556;
OS Corynebacterium diptheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Biotype Gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cerdeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
RA Fallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Hollroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinovitch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RT "The complete genome sequence and analysis of Corynebacterium
RT diptheriae NCTC13129."
RL Nucleic Acids Res. 31:6516-6523 (2003).
DR EMBL; BX249355; CAE49068.1; -.
DR GO; GO:000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 2.
DR SMART; SM00382; AAA; 3.
DR PROSITE; PS50901; FTSK; 3.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 1179 AA; 128991 MW; 2939055714E35A69 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1179;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPFATELHE 11
Db 931 KLQPTAVELHE 941

RESULT 18
TNF5_RAT STANDARD; PRT; 260 AA.
AC Q922V2; Q9R254;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L).
GN Names=Tnfrsf5; Synonyms=Cd40l, Cd40lg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Splenocyte;

```

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RX MEDLINE=20284949; PubMed=10826698;
RA Hallatt K.M., Oaks M.K.;
RT "Nucleotide sequence of the rat CD40 ligand.";
RL DNA Seq. 10:405-406 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG; TISSUE=Spleen;
RA Daniel K.C., Foss Y., Mousavi A., Macary P., Kemeny D.M.,
RA Farzaneh F., Gaken J.A.;
RT "Cloning and sequencing of rat CD40 ligand.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IGE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF116582; AAD22460.1; -.
CC EMBL; AF013985; AAD09323.1; -.
CC HSSP; P29965; ITALY.
CC RGD; 708418; LOC84349.
CC GO; GO:0016021; C:integral to membrane; ISS.
CC GO; GO:0003174; F:CD40 receptor binding; ISS.
CC GO; GO:0042100; P:B-cell proliferation; ISS.
CC GO; GO:0006954; P:inflammatory response; ISS.
CC GO; GO:0007159; P:leukocyte cell adhesion; ISS.
CC GO; GO:0030168; P:platelet activation; ISS.
CC InterPro; IPR003263; TNF_5.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC Pfam; PF00229; TNF; 1.
CC InterPro; IPR003636; TNF_subf.
CC PRINTS; PR01702; CD40LIGAND.
CC ProDom; PD008600; TNF_5; 1.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Glycoprotein; Signal-anchor; Transmembrane.
FT CHAIN 1 260
FT CHAIN 112 260
FT DOMAIN 1 22
FT TRANSMEM 23 43
FT DOMAIN 44 260
FT SITE 111 112
FT DISULFID 177 217
FT CARBOHYD 239 239
FT CONFLICT 41 41
FT CONFLICT 114 114
FT CONFLICT 255 255
FT SEQUENCE 260 AA; 29259 MW; B3D3757DE60DB73A CRC64;
SQ
Query Match 60.6%; Score 40; DB 1; Length 260;
Best Local Similarity 72.7%; Pred. No. 81;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 VFPATELHERL 13

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||||| ||| |||
40 VPFVYLHREL 50

Db

RESULT 19

APAL RABIT
ID APAL RABIT STANDARD; PRT; 266 AA.
AC P09809;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Apolipoprotein A-I precursor (Apo-AI).
GN Names=APOA1;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22AP AI; TISSUE=Small intestine;
RA Paraskevopoulou T.B., Kritis A., Zannis V.I.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=88082866; PubMed=3121329;
RA Pan T.C., Hao Q.L., Yamin T.T., Dai P.H., Chen B.S., Chen S.L.,
RA Kroon P.A., Chao Y.S.;
RT "Rabbit apolipoprotein A-I mRNA and gene. Evidence that rabbit
RT apolipoprotein A-I is synthesized in the intestine but not in the
RT liver.";
RL Eur. J. Biochem. 170:99-104 (1987).
RN [3]
RP SEQUENCE OF 25-266.
RX MEDLINE=87030294; PubMed=3095115;
RA Yang C., Yang T., Pownall H.J., Gotto A.M. Jr.;
RT "The primary structure of apolipoprotein A-I from rabbit high-density
RT lipoprotein";
RL Eur. J. Biochem. 160:427-431 (1986).
CC -1- FUNCTION: Participates in the reverse transport of cholesterol
CC from tissues to the liver for excretion by promoting cholesterol
CC efflux from tissues and by acting as a cofactor for the lecithin
CC cholesterol acyltransferase (LCAT).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Major protein of plasma HDL, also found in
CC chylomicrons.
CC -1- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X15908; CAA34024.1; --
CC EMBL; X06658; CAA29857.1; --
CC EMBL; X06659; CAA29858.1; --
CC PIR; S06064; LPRB12.
CC HSP; P02647; IAV1.
CC InterPro; IPR009074; Apolipo_A_E_C3.
CC InterPro; IPR000074; Apolipoprotein.
CC Pfam; PF01442; Apolipoprotein; 1.
CC Cholesterol metabolism; Direct protein sequencing; HDL;
CC Lipid transport; Plasma; Repeat; Signal.
CC SIGNAL 1 18
CC PROPEP 19 24 Apolipoprotein A-I.
CC CHAIN 25 266 10 X approximate tandem repeats.
CC DOMAIN 67 266 1.
CC REPEAT 67 88 1.
CC REPEAT 89 110 2.
CC REPEAT 111 121 3 (half-length).
CC

FT REPEAT 122 143 4.
FT REPEAT 144 165 5.
FT REPEAT 166 187 6.
FT REPEAT 188 209 7.
FT REPEAT 210 231 8.
FT REPEAT 232 242 9. (half-length).
FT REPEAT 243 266 10.
FT CONFLICT 18 18 A -> R (in Ref. 2; CAA29858).
FT CONFLICT 44 44 Missing (in Ref. 3).
FT CONFLICT 45 45 V -> I (in Ref. 2; CAA29858).
FT CONFLICT 107 107 E -> Q (in Ref. 3).
FT CONFLICT 123 123 Y -> F (in Ref. 2; CAA29857).
FT CONFLICT 147 147 A -> V (in Ref. 2; CAA29858 and 3).
FT CONFLICT 150 150 R -> G (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 191 191 N -> Q (in Ref. 3).
FT CONFLICT 195 195 Missing (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 211 211 S -> K (in Ref. 2; CAA29858/CAA29857).
FT CONFLICT 255 255 VL -> LV (in Ref. 3).
FT CONFLICT 256 256 L -> V (in Ref. 2; CAA29858/CAA29857).
SQ SEQUENCE 266 AA; 30591 MW; 0FF6DB386497C7D2 CRC64;
Query Match 60.6%; Score 40; DB 1; Length 266;
Best Local Similarity 53.8%; Pred No. 83;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLVPPFATELHERL 13
DB 185 KLPYSNELQRL 197
RESULT 20
Q66IL6 PRELIMINARY; PRT; 368 AA.
AC Q66IL6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081300; AAH81300.1; --.


```
DR InterPro; IPR000074; Apolipoprotein.
DR InterPro; IPR009074; Apolipo A E C3.
DR Pfam; PF01442; Apolipoprotein; 1.
KW Hypothetical protein.
SQ SEQUENCE 368 AA; 42501 MW; C4EA22D395FC9DB4 CRC64;

  Query Match      60.6%; Score 40; DB 2; Length 368;
  Best Local Similarity 38.5%; Pred. No. 1.2e+02;
  Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
   :::|||::|:|:|
DB 79 QVIFPAKIHQDL 91

RESULT 21
Q6CGG7 PRELIMINARY; PRT; 585 AA.
AC Q6CGG7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to tr|Q06436 Saccharomyces cerevisiae YJR427w.
GN ORFNames=YAL10A19149;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
[2]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; CR382127; CAG84183.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING 1; 1.
DR PROSITE; PS50089; ZF_RING 2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 585 AA; 65101 MW; BAA6D587D0F92CD2 CRC64;

  Query Match      60.6%; Score 40; DB 2; Length 585;
  Best Local Similarity 66.7%; Pred. No. 1.8e+02;
  Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPPFATELHER 12
   || ||| ||| :|
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Db 439 KLPFAELKQR 450

RESULT 22
Q7ULM6 PRELIMINARY; PRT; 656 AA.
ID Q7ULM6;
AC Q7ULM6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB9405;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RA "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294149; CAD76243.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 656 AA; 75050 MW; 977C8888D2510F02 CRC64;

  Query Match      60.6%; Score 40; DB 2; Length 656;
  Best Local Similarity 70.0%; Pred. No. 2.1e+02;
  Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPFATELHER 12
   :||| ||| |||
DB 255 LPFITSLHER 264

RESULT 23
Q7N819 PRELIMINARY; PRT; 150 AA.
ID Q7N819;
AC Q7N819;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to unknown protein.
GN OrderedLocusNames=plu0929;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Pasesa E., Berose R., Derzelle S., Freysinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Signier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571862; CAE13224.1; -.
DR PhotoList; plu0929; -.
DR InterPro; IPR002716; Pilt_N.
DR Pfam; PF01850; PIN; 1.
KW Complete proteome.
SQ SEQUENCE 150 AA; 17131 MW; 7FBE5C3A2B05F3D8 CRC64;

  Query Match      59.1%; Score 39; DB 2; Length 150;
  Best Local Similarity 50.0%; Pred. No. 71;
```


Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 KLVPFATELHER 12
DB 86 KIVPLTVEVHDR 97

RESULT 24

Q8GF72 PRELIMINARY; PRT; 177 AA.
AC Q8GF72; (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Orf75;
GN Name=orf75;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=21185117; PubMed=11286884; DOI=10.1016/S0966-842X(01)01978-3;
RA Waterfield N.R., Bowen D.J., Fetherston J.D., Perry R.D.,
french-Constant R.H.;
RT "The tc genes of Photorhabdus: a growing family";
RL Trends Microbiol. 9:185-191(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
RA Waterfield N.R., Daborn P.J., french-Constant R.H.;
RT "Genomic islands in Photorhabdus";
RL Trends Microbiol. 10:541-545(2002).
DE EMBL; AF346500; AA017229.1; -;
DR InterPro; IPR002716; Pilt N.
DR InterPro; IPR006596; Pinc.
DR Pfam; PF01850; PIN; 1.
DR SMART; SM00670; PIN; 1.
SQ SEQUENCE 177 AA; 19857 MW; 31C279D8D49172B9 CRC64;

Query Match 59.1%; Score 39; DB 2; Length 177;
Best Local Similarity 50.0%; Pred. No. 84;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLVPFATELHER 12
DB 113 KIVPLTVEVHDR 124

RESULT 25

Q830L3 PRELIMINARY; PRT; 220 AA.
AC Q830L3;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Transcriptional regulator.
GN OrderedLocusNames=EF2767;
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,
Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,
Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,

Fraser C.M.;
RA "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis";
RL Science 299:2071-2074(2003).
DE EMBL; AE016955; AA082465.1; -;
DR TIGR; EF2767; -;
DR InterPro; IPR004305; TENA_THI-4.
DR Pfam; PF03070; TENA_THI-4; 1.
KW Complete proteome.
SQ SEQUENCE 220 AA; 25626 MW; 1024606E58E24D4F CRC64;

Query Match 59.1%; Score 39; DB 2; Length 220;
Best Local Similarity 87.5%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PFATELHE 11
DB 22 PFITELHE 29

RESULT 26

P87210 PRELIMINARY; PRT; 353 AA.
AC P87210;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MEI3.
GN Name=mei-3;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A; PubMed=8552049;
RX MEDLINE=96133684; Hatakeyama S., Ishii C., Inoue H.;
RA Hatakeyama S., Ishii C., Inoue H.;
RT "Identification and expression of the Neurospora crassa mei-3 gene
RT which encodes a protein homologue to Rad51 of Saccharomyces
cerevisiae";
RL Mol. Gen. Genet. 249:439-446(1995).
CC -1- SIMILARITY: Belongs to the reca family.
DE EMBL; D29638; BAA20366.1; -;
DR PIR; S70629; S70629.
DR HSP; Q06609; INOW.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003684; F:damaged DNA binding; IEA.
DR GO; GO:0008094; F:DNA-dependent ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006281; P:DNA repair; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR000445; Hhh.
DR InterPro; IPR003583; Hhh 1.
DR InterPro; IPR010995; Rad51_N.
DR InterPro; IPR001553; RecA.
DR Pfam; PF00633; Hhh; 1.
DR ProDom; PD000229; RecA; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00278; Hhh1; 1.
DR PROSITE; PS50162; RECA_2; 1.
DR PROSITE; PS50163; RECA_3; 1.
KW ATP-binding.
SQ SEQUENCE 353 AA; 38202 MW; B79DC4D2DA0B8548 CRC64;

Query Match 59.1%; Score 39; DB 2; Length 353;
Best Local Similarity 56.2%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 KLVPF---ATELHER 12
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Db      84 KLVPMTGFTATEMHQR 99

RESULT 27
Q9CA19  PRELIMINARY;      PRT;      697 AA.
AC Q9CA19;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F28222.5.
GN Name=F28222.5;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.J.,
RA Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.,
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Town C.D., Kaul S.,
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AC010926; AGS1852.1; -.
DR PIR; E96752; E96752.
DR HSSP; Q62838; ILUF.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin_AS.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 697 AA; 77917 MW; 67C01D858364BE5 CRC64;

Query Match      59.1%; Score 39; DB 2; Length 697;
Best Local Similarity 61.5%; Pred. No. 3.3e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 KLVPMTGFTATEMHQR 13
Db      647 RLKEFATEDHERI 659

RESULT 28
Q7R3A9  PRELIMINARY;      PRT;      2710 AA.
AC Q7R3A9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE GLP 111.35594.43726.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RL "draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
```

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CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
DR EMBL; AACB01000016; EAA41809.1; -.
DR GO; GO:0030286; C:dynenin complex; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004273; Dynein_heavy.
DR InterPro; IPR000897; SRP54.
DR Pfam; PF03028; Dynein_heavy; 1.
DR PROSITE; PS00300; SRP54; UNKNOWN_1.
SQ SEQUENCE 2710 AA; 303764 MW; 35CC068501F67345 CRC64;

Query Match      59.1%; Score 39; DB 2; Length 2710;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 KLVPFATELHE 11
Db      1022 RLAPIATEIHD 1032

RESULT 29
Q48926  PRELIMINARY;      PRT;      2796 AA.
AC Q48926;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid synthase.
GN Name=fas;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCG-Pasteur;
RX MEDLINE=96200863; PubMed=8621098; DOI=10.1016/0378-1119(95)00842-X;
RA Fernandes N.D., Kolattukudy P.E.;
RT "Cloning, sequencing and characterization of a fatty acid synthase-
RT encoding gene from Mycobacterium tuberculosis var. bovis BCG.";
RL Gene 170:95-99(1996).
DR EMBL; U36763; AAB03809.1; -.
DR PIR; JC4743; JC4743.
DR GO; GO:0005835; C:fatty-acid synthase complex; IEA.
DR GO; GO:0004312; F:fatty-acid synthase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac_transferase.
DR InterPro; IPR003965; Fatty_acid_synth.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR002539; MaoC_dehydratas.
DR Pfam; PF00698; Acyl_transf_1; 1.
DR Pfam; PF00109; ketoacyl-synt_1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR Pfam; PF01575; MaoC_dehydratas; 1.
DR PRINTS; PR01483; FASYNTHASE.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
KW Transferase.
SQ SEQUENCE 2796 AA; 303676 MW; 47B87169126D2504 CRC64;

Query Match      59.1%; Score 39; DB 2; Length 2796;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 PFATELHERL 13
Db      2755 PNETELHERL 2764
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RN  SEQUENCE FROM N.A.
RP  STRAIN=H37RV;
RX  MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
RA  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RA  Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
RA  Tekala F., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RA  Connor R., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RA  Holroyd S., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RA  Murphy L.D., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA  Rogers J., Rutter S., Taylor K., Whitehead S., Barrell B.G.;
RA  "Deciphering the biology of Mycobacterium tuberculosis from the
RT  complete genome sequence.";
RL  Nature 393:537-544(1998).
DR  EMBL; BX842580; CAB06201.1; -.
DR  PIR; H70656; H70656.
DR  TubercuList; RV2524c; -.
DR  GO; GO:0005835; C:fatty-acid synthase complex; IEA.
DR  GO; GO:0004312; F:fatty-acid synthase activity; IEA.
DR  GO; GO:0016491; F:oxidoreductase activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro; IPR001227; Ac_transferase.
DR  InterPro; IPR003965; Fatty_acid_synth.
DR  InterPro; IPR000794; Ketoacyl_synth.
DR  InterPro; IPR002539; MaaC_dehydratase.
DR  Pfam; PF00698; Acyl_transf_1; 1.
DR  Pfam; PF00109; Ketoacyl-synt; 1.
DR  Pfam; PF02801; Ketoacyl-synt C; 1.
DR  Pfam; PF01575; MaaC_dehydratase; 1.
DR  PRINTS; PR01483; FASYNTHASE.
DR  PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN 1.
KW  Acyltransferase; Complete proteome; Transferase.
SQ  SEQUENCE 3069 AA; 326251 MW; 25EF022D54943D4C CRC64;

Query Match 59.1%; Score 39; DB 2; Length 3069;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  4 PFATLHERL 13
Db  2881 PNETLHERL 2890

RESULT 32
Q7TYD8 PRELIMINARY; PRT; 3069 AA.
AC Q7TYD8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PROBABLE FATTY ACID SYNTHASE FAS (FATTY ACID SYNTHETASE) (EC 2.3.1.-
DE ).
GN Name=fas; OrderedLocusNames=MD2553c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garner T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RA "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248342; CAD97414.1; -.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.

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DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001227; AC:transferase.
 DR InterPro; IPR000794; Ketoacyl_synth.
 DR InterPro; IPR002539; Maoc dehydratas.
 DR Pfam; PF00698; Acyl_transf_1; 1.
 DR Pfam; PF00109; ketoacyl-synt_C; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF01575; Maoc dehydratas; 1.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR Acyltransferase; Complete proteome; Transferase.
 KW ACYLTRANSFERASE; Complete proteome; Transferase.
 SQ SEQUENCE 3069 AA; 326304 MW; 6855667940C025A2 CRC64;

Query Match 59.1%; Score 39; DB 2; Length 3069;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
 | | | | | | | |
 Db 2881 PNETELHERL 2890

RESULT 33

Q9X7E2 PRELIMINARY; PRT; 3076 AA.
 AC Q9X7E2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Fatty acid synthase.
 GN Name-fas; OrderedLocusNames=ML1191;
 OS Mycobacterium leprae.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93188700; PubMed=8446027;
 RA Eiglmeyer K., Honore N., Woods S.A., Caudron B., Cole S.T.;
 RT "use of an ordered cosmid library to deduce the genomic organization
 of Mycobacterium leprae.";
 RL Mol. Microbiol. 7:197-206(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Seeger K.J., Harris D.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TN;
 RX MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006;
 RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E.,
 RA Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 RL EMBL; AL049478; CAB39571.1; -
 DR EMBL; AL583921; CAB31572.1; -
 DR EMBL; A87058; A87058.
 DR HSSP; P25715; IMLA.
 DR Leproma; ML1191; -
 DR GO; GO:0005835; C:fatty-acid synthase complex; IEA.
 DR GO; GO:0004312; F:fatty-acid synthase activity; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001227; AC:transferase.
 DR InterPro; IPR003965; Fatty_acid_synth.
 DR InterPro; IPR000794; Ketoacyl_synth.
 DR InterPro; IPR002539; Maoc dehydratas.
 DR Pfam; PF00698; Acyl_transf_1; 1.
 DR Pfam; PF00109; ketoacyl-synt_C; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF01575; Maoc dehydratas; 1.
 DR PROSITE; PS01483; FASYNTHASE.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR Complete proteome; Transferase.
 KW COMPLETE PROTEOME; Transferase.
 SQ SEQUENCE 3076 AA; 328358 MW; D88556730478E549 CRC64;

Query Match 59.1%; Score 39; DB 2; Length 3076;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
 | | | | | | | |
 Db 2888 PNETELHERL 2897

RESULT 34

Q73XH7 PRELIMINARY; PRT; 3092 AA.
 AC Q73XH7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Fas.
 GN Name-fas; OrderedLocusNames=MAP2332c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=K10;
 RC Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE017235; AAS04649.1; -
 DR GO; GO:0005835; C:fatty-acid synthase complex; IEA.
 DR GO; GO:0004312; F:fatty-acid synthase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001227; AC:transferase.
 DR InterPro; IPR003965; Fatty_acid_synth.
 DR InterPro; IPR002114; HPT_SerP_S.
 DR InterPro; IPR000794; Ketoacyl_synth.
 DR InterPro; IPR002539; Maoc dehydratas.
 DR Pfam; PF00698; Acyl_transf_1; 1.
 DR Pfam; PF00109; ketoacyl-synt_C; 1.
 DR Pfam; PF02801; ketoacyl-synt_C; 1.
 DR Pfam; PF01575; Maoc dehydratas; 1.
 DR PROSITE; PS01483; FASYNTHASE.
 DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR Complete proteome; Transferase.
 KW COMPLETE PROTEOME; Transferase.
 SQ SEQUENCE 3092 AA; 328070 MW; 3616EDD7DF0350D9 CRC64;

Query Match 59.1%; Score 39; DB 2; Length 3092;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PFATELHERL 13
 | | | | | | | |
 Db 2901 PNETELHERL 2910

Query Match 57.6%; Score 38; DB 2; Length 162;
 Best Local Similarity 61.5%; Pred. No. 1.2e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KLVPPFATELHERL 13
 Db 126 KIVPFALERETRL 138

RESULT 37
 Q6HCP9 PRELIMINARY; PRT; 176 AA.
 ID Q6HCP9
 AC Q6HCP9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=BT9727_4362;
 OS Bacillus thuringiensis (Subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=180856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-27;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017355; AAF60913.1; -;
 KW Complete proteome.
 SQ SEQUENCE 176 AA; 20899 MW; C2BFA22CCB7F18A8 CRC64;

Query Match 57.6%; Score 38; DB 2; Length 176;
 Best Local Similarity 54.5%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLVPPFATELHE 11
 Db 75 KNAPFSTEIHD 85

RESULT 38
 Q9X548 PRELIMINARY; PRT; 250 AA.
 ID Q9X548
 AC Q9X548;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
 DE Yag1C.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OG Plasmid R-plasmid PAG1.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 ON NCBI_TaxID=1718;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22243;
 RX MEDLINE=20532766; PubMed=11078655; DOI=10.1006/plas.2000.1489;
 RA Tauch A., Puhler A., Kallinowski J., Thierbach G.;
 RT "TetZ, a new tetracycline resistance determinant discovered in gram-positive bacteria, shows high homology to gram-negative regulated efflux systems";
 RL Plasmid 44:285-291 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22243;
 RA Tauch A.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF121000; AAD25067.1; -;
 KW Plasmid.
 SQ SEQUENCE 250 AA; 27505 MW; 436F69A27AFA9DBF CRC64;

RESULT 35

Q6K305 PRELIMINARY; PRT; 57 AA.

ID Q6K305
 AC Q6K305;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSJNB00666C12.39.
 GN Names=OSJNB00666C12.39;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 ON NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC
 RT clone: OSJNB00666C12.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005738; BAD23565.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 57 AA; 6414 MW; 723678FE6D6828F6 CRC64;

Query Match 57.6%; Score 38; DB 2; Length 57;
 Best Local Similarity 80.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LVPFATELHE 11
 Db 6 LVPFATELHE 15

RESULT 36
 Q89SR9 PRELIMINARY; PRT; 162 AA.
 ID Q89SR9
 AC Q89SR9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transcriptional regulatory protein.
 GN OrderedLocNames=blr2331;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 ON NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpou S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197 (2002).
 CC -1- SIMILARITY: Contains 1 HTH marR-type DNA-binding domain.
 DR EMBL; AP005943; BAC47596.1; -;
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000835; HTH_MarR.
 DR InPro; IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam; PF01047; MarR.1
 DR PRINTS; PR00598; HTHMARR.
 DR SMART; SM00347; HTH_MARR.1.
 KW Complete proteome; DNA-binding; Transcription;
 Transcription regulation.
 SQ SEQUENCE 162 AA; 18163 MW; PAE5DAB4137F535A CRC64;

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Query Match 57.6%; Score 38; DB 2; Length 250;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PFATELHE 11
DB 202 PFADLHE 209

RESULT 39
ID O33624 PRELIMINARY; PRT; 288 AA.
AC O33624;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Orf5yn (Fragment).
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M145;
RA Burger A., Wohleben W.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, Y14206; CAA74602.1;
DR InterPro; IPR000834; Peptidase_M14.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31935 MW; A20726737132F121 CRC64;

Query Match 57.6%; Score 38; DB 2; Length 288;
Best Local Similarity 58.3%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LVPFATELHERL 13
DB 273 LVPLAETVHERM 284

RESULT 40
ID O6GK71 PRELIMINARY; PRT; 311 AA.
AC O6GK71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative inosine-uridine preferring nucleoside hydrolase.
GN OrderedLocNames-SAR0236;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.04025211101;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster I.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Maves R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL; BX571856; CAG39263.1;
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001910; I/U_nucleid_hydro.
DR Pfam; PF01156; IU_nuc_hydro; 1.
DR ProDom; PD007736; I/U_nucleid_hydro; 1.
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DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS01247; IUNH; 1.
KW Complete proteome.
SQ SEQUENCE 311 AA; 33881 MW; FC8A3429B4309D6A CRC64;

Query Match 57.6%; Score 38; DB 2; Length 311;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLVPFATELH 10
DB 74 KLVAFASEIH 83

RESULT 41
ID O6RWS4 PRELIMINARY; PRT; 314 AA.
AC O6RWS4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nitrilase (EC 3.5.5.7).
GN ORFNames=BD7612;
OS uncultured organism.
OX unclassified; environmental samples.
OX NCBI_TaxID=155900;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15066841; DOI=10.1128/AEM.70.4.2429-2436.2004;
RA Robertson D.E., Chaplin J.A., DeSantis G., Fodor M., Madden M.,
RA Chi E., Richardson T., Milan A., Miller M., Weiner D.P., Wong K.,
RA McQuaid J., Farrell B., Preston L.A., Tan X., Sneed M.A., Keller M.,
RA Mathur E., Kretz P.L., Burk M.J., Short J.M.;
RT "Exploring nitrilase sequence space for enantioselective catalysis.";
RL Appl. Environ. Microbiol. 70:2429-2436(2004).
DR EMBL; AY487428; AAR97375.1;
DR GO; GO:0018762; F:aliphatic nitrilase activity; IEA.
DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. .; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR000132; N/CN_hydrolase.
DR InterPro; IPR003010; Ntase/CNhydrtase.
DR Pfam; PF00795; CN_hydrolase; 1.
DR PROSITE; PS0263; CN_HYDROLASE; 1.
DR PROSITE; PS00920; NITRIL_CHT_1; 1.
KW Hydrolase.
SQ SEQUENCE 314 AA; 34391 MW; B6C814543EC19B83 CRC64;

Query Match 57.6%; Score 38; DB 2; Length 314;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 VPFATELHERL 13
DB 63 VKLAELHERL 73

RESULT 42
ID O66538 PRELIMINARY; PRT; 317 AA.
AC O66538;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ADP-heptose-LPS heptosyltransferase.
GN Name=rfac2; OrderedLocNames=AQ_145;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland I., Young W.G., Lenox A.L.,
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Query Match 57.6%; Score 38; DB 2; Length 317;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VFATLHE 11
158 VFATMVHE 166

RESULT	45
Q6R315	PRELIMINARY; PRT; 335 AA.
ID	Q6R315
AC	Q6R315;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Conserved protein.
OS	Gemmata sp. Wal-1.
OC	Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC	Planctomycetaceae; Gemmata.
OX	NCBI_TaxID=235140;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	PubMed=15014146; DOI=10.1093/molbev/msh113;
RA	Chistosodova L., Jenkins C., Kalyuzhnaya M.G., Marx C.J., Lapidus A.,
RA	Vorholt J.A., Staley J.T., Lidstrom M.E.;
RT	"The enigmatic planctomycetes may hold a key to the origins of methanogenesis and methyotrophy.";
RL	Mol. Biol. Evol. 21:1234-1241(2004).
RM	EMBL; AY515680; AAC88969.1; -.
DR	GO; GO:0016787; F:hydrolase activity; IEA.
DR	InterPro; IPR002756; DUF66.
DR	InterPro; IPR002821; Hydantoinase A.
DR	Pfam; PF01968; Hydantoinase A; 1.
DR	pCDOm; PD024636; DUF66; 1.
DR	SEQUENCE 335 AA: 36242 MW: D0094C3791B10372 CRC64;

Query Match 57.6%; Score 38; DB 2; Length 335;
Best Local Similarity 46.2%; Pred. No. 2.4e+02;
Matches 6: Conservative 4; Mismatches 3; Indels

244 QIHFATRIHSRL 256

Search completed: September 1, 2005, 16:40:43
Job time : 178 secs

OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.

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